

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 30, 2003, 15:03:47 ; Search time 38 seconds

(without alignments)
1451.730 Million cell updates/sec

Title: US-09-990-087-17

Perfect score: 2118

Sequence: 1 MGHHHHHIEGRLLKLDND.....SFKVSFSLAEYTKKLNTQ 414

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1024	48.3	243	9 AAP81082	Sequence of mature
2	1024	48.3	267	7 AAP61079	Assumed human apol
3	1024	48.3	267	9 AAP82128	Entire human prepr
4	1024	48.3	267	14 AAR34032	Sequence of apo AI
5	1024	48.3	267	16 AAR72705	Human apo A-I incl
6	1024	48.3	267	20 AAY18675	Human apolipoprote
7	1024	48.3	267	22 AAB47620	Full length Apo-AI
8	1024	48.3	267	9 AAP80668	Recombinant human
9	1016	48.0	268	18 AAW08602	Human apolipoprote
10	1014	47.9	264	15 AAR56863	Apo-lipoprotein AI

11	1014	47.9	264	15	AAR56864	Apo-lipoprotein AI
12	990	46.7	299	22	AAU33170	Novel human secret
13	974	46.0	244	22	AAU28184	Novel human secret
14	788	37.2	221	22	AAU29835	Novel human secret
15	726.5	34.3	318	22	AAU30268	Novel human secret
16	643	30.4	359	22	AAU30470	Novel human secret
17	635	30.0	151	22	AAU02278	Human polypeptide
18	541	25.5	119	22	AAU04668	Novel human secret
19	526	24.8	166	22	AAU28372	Novel human secret
20	355	16.8	120	22	AAU30267	Novel human secret
21	355	16.8	120	22	AAU30469	Novel human secret
22	349.5	16.5	373	14	AAR39486	Human apoAIV mutei
23	339	16.0	337	14	AAR39485	Human apoAIV mutei
24	335	15.8	342	14	AAR39487	Human apoAIV mutei
25	324.5	15.3	396	22	AAB90664	Human secreted pro
26	323.5	15.3	363	14	AAR39479	Human apoAIV mutei
27	323.5	15.3	377	14	AAR39443	Human apolipoprote
28	323.5	15.3	377	14	AAR39502	Human apoAIV mutei
29	323.5	15.3	377	14	AAR39501	Human apoAIV mutei
30	321.5	15.2	396	23	AAU10863	Human apolipoprote
31	320.5	15.1	377	14	AAR39499	Human apoAIV mutei
32	320.5	15.1	377	14	AAR39500	Human apolipoprote
33	320.5	15.1	396	23	AAU10860	Human apoAIV mutei
34	320.5	15.1	396	23	AAU10861	Human apolipoprote
35	320.5	15.1	396	23	AAU10865	Human apolipoprote
36	320.5	15.1	396	23	AAU10867	Human apolipoprote
37	320.5	15.1	396	23	AAU10868	Human apolipoprote
38	320.5	15.1	396	23	AAU10869	Human apolipoprote
39	319.5	15.1	363	14	AAR39478	Human apoAIV mutei
40	319.5	15.1	377	14	AAR39480	Human apoAIV mutei
41	319.5	15.1	377	14	AAR45244	Human apoAIV mutei
42	319.5	15.1	396	23	AAU10864	Human apolipoprote
43	318.5	15.0	377	14	AAR45243	Human apoAIV mutei
44	318.5	15.0	396	23	AAU10866	Human apolipoprote
45	317.5	15.0	333	14	AAR39481	Human apoAIV mutei

ALIGNMENTS

```
RESULT 1
AAP81082
ID AAP81082 standard; protein; 243 AA.
XX
AC AAP81082;
XX
DT 14-JAN-1991 (first entry)
XX
DE Sequence of mature human apolipoprotein AI (apoAI).
XX
KW Atherosclerosis; therapy; cardiovascular disease.
XX
OS Homo sapiens.
XX
PN WO8803166-A.
XX
PD 05-MAY-1988.
XX
PF 21-OCT-1987; 87WO-EP00621.
XX
PR 23-OCT-1986; 86GB-0025435.
XX
(PARM ) FARMITALIA C ERBA SPA.
XX
PI Lorenzetti R, Monaco L, Soria M, Palomba R, Isacchi A, Sarmientos P;
XX
WPI; 1988-133240/19.
XX
N-PSDB; AAN80243.
XX
Recombinant human apo-lipoprotein AI -
XX
used to lower plasma cholesterol and/or tri glyceride levels and
XX
to combat atherosclerosis and cardiovascular diseases
```

PS Disclosure; Fig 1; 5lpp; English.

XX The protein comprising apo AI genetic variants may be used to lower
 CC plasma cholesterol and/or triglyceride levels. They may also be used to
 CC combat atherosclerosis and cardiovascular diseases such as coronary
 CC heart disease. Pred. proteins are Met-apo AI, Met-apo AI-r6, Met-apo
 CC AI-MI and Met-apo AI-r6/MI.

XX Sequence 243 AA;

Query Match 48.3%; Score 1024; DB 9; Length 243;

Best Local Similarity 88.5%; Pred. No. 2.2e-60;

Matches 208; Conservative 6; Mismatches 19; Indels 2; Gaps 1;

QY 180 LEDRQGLLPVLESFKVSVLSALEEYTKKLTQGTCLKLDNWDVSTSTFSKLRQLGPVT 239

DB 11 VKDLATVYDVILKSDGRDYVSQFE--GSALGKQLNLKLDNWDVSTSTFSKLRQLGPVT 68

QY 240 QEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQE 299

DB 69 QEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQE 128

QY 300 GARQKLHELQEKLSPLGEEMDRARAHVDALRTHLAPYSDELQRQLAARLEALKENGAR 359

DB 129 GARQKLHELQEKLSPLGEEMDRARAHVDALRTHLAPYSDELQRQLAARLEALKENGAR 188

QY 360 LAEYHAKATEHLSTLSEKAKPALEDLROGLLPVLESFKVSVLSALEEYTKKLTQ 414

DB 189 LAEYHAKATEHLSTLSEKAKPALEDLROGLLPVLESFKVSVLSALEEYTKKLTQ 243

RESULT 2

AAP61079

ID AAP61079 standard; Protein; 267 AA.

XX AAP61079;

DT 07-OCT-1991 (first entry)

XX Assumed human apolipoprotein A-1 derivative gene product.

DE Hyperlipaemia; arteriosclerosis.

KW Homo sapiens.

OS JP61096998-A.

PN 15-MAY-1986.

PD 16-OCT-1984; 84JP-0216988.

PF 16-OCT-1984; 84JP-0216988.

PT (MITU) MITSUBISHI CHEM IND KK.

XX WPI; 1986-165025/26.

XX N-PSDB; AAN60886.

XX Human apo:lipoprotein A-1 (deriv.) prepn. - by providing DNA

PT fragment in cloning site downstream of expression vector promoter

PT and introducing into host microorganism.

XX Disclosure; Fig 2; 9pp; Japanese.

PS The human apolipoprotein may be produced by a suitable transformed

CC host, it is effective in treating hyperlipaemia and arteriosclerosis.

XX Sequence 267 AA;

Query Match 48.3%; Score 1024; DB 7; Length 267;

Best Local Similarity 88.5%; Pred. No. 2.5e-60;

Matches 208; Conservative 6; Mismatches 19; Indels 2; Gaps 1;

QY 180 LEDRQGLLPVLESFKVSVLSALEEYTKKLTQGTCLKLDNWDVSTSTFSKLRQLGPVT 239

DB 35 VKDLATVYDVILKSDGRDYVSQFE--GSALGKQLNLKLDNWDVSTSTFSKLRQLGPVT 92

QY 180 LEDRQGLLPVLESFKVSVLSALEEYTKKLTQGTCLKLDNWDVSTSTFSKLRQLGPVT 239

DB 35 VKDLATVYDVILKSDGRDYVSQFE--GSALGKQLNLKLDNWDVSTSTFSKLRQLGPVT 92

QY 240 QEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQE 299

DB 93 QEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQE 152

QY 300 GARQKLHELQEKLSPLGEEMDRARAHVDALRTHLAPYSDELQRQLAARLEALKENGAR 359

DB 153 GARQKLHELQEKLSPLGEEMDRARAHVDALRTHLAPYSDELQRQLAARLEALKENGAR 212

QY 360 LAEYHAKATEHLSTLSEKAKPALEDLROGLLPVLESFKVSVLSALEEYTKKLTQ 414

DB 213 LAEYHAKATEHLSTLSEKAKPALEDLROGLLPVLESFKVSVLSALEEYTKKLTQ 267

RESULT 3

AAP82128

ID AAP82128 standard; protein; 267 AA.

XX AAP82128;

DT 24-OCT-1990 (first entry)

XX Entire human preproapoprotein A1.

DE human preproapoprotein A1; high density lipoprotein deficiency; ss.

KW synthetic.

OS Key

FH Location/Qualifiers

FT Peptide 1..18

FT Peptide /label=precursor

FT Peptide 19..24

FT Peptide /label=propeptide

FT Protein 25..267

FT /label=mature apoprotein

XX EP293357-A.

XX 30-NOV-1988.

XX 24-MAY-1988; 88EP-0870095.

XX 28-MAY-1987; 87GB-0012540.

XX (UNIO) UCB SA.

XX Bollen A, Gobert J, Wulfert E;

XX WPI; 1988-339891/48.

XX N-PSDB; AAN82064.

XX New DNA encoding human preproapoprotein A1 -

PT modified to eliminate hairpin structures

XX Disclosure; ; p; French.

XX The cDNA 878bp fragment encoding preproapoprotein A1 was detected

CC in clone pULB1609 derived from human liver cells.

CC See also AAN81258.

XX Sequence 267 AA;

Query Match 48.3%; Score 1024; DB 9; Length 267;

Best Local Similarity 88.5%; Pred. No. 2.5e-60;

Matches 208; Conservative 6; Mismatches 19; Indels 2; Gaps 1;

QY 180 LEDRQGLLPVLESFKVSVLSALEEYTKKLTQGTCLKLDNWDVSTSTFSKLRQLGPVT 239

DB 35 VKDLATVYDVILKSDGRDYVSQFE--GSALGKQLNLKLDNWDVSTSTFSKLRQLGPVT 92

QY 240 QEFWDNLEKETEGRLQEMSKDLEEVKAKVQPYLDLDFOKKQWQEMELYRQKVEPLRAELQ 299
 DB 93 QEFWDNLEKETEGRLQEMSKDLEEVKAKVQPYLDLDFOKKQWQEMELYRQKVEPLRAELQ 152

QY 300 GARQKLHELOEKLSPGLGEMDRARAHVDALRTHLAPYSDELQRLAARLEALKENGAR 359
 DB 153 GARQKLHELOEKLSPGLGEMDRARAHVDALRTHLAPYSDELQRLAARLEALKENGAR 212

QY 360 LAEYHAKATEHLSTLSEKAKPALEDLROGLLPVLESKVSVLSALEEYTKKLNTQ 414
 DB 213 LAEYHAKATEHLSTLSEKAKPALEDLROGLLPVLESKVSVLSALEEYTKKLNTQ 267

RESULT 4
 AAR34032
 ID AAR34032 standard; Protein; 267 AA.
 XX
 AC AAR34032;
 XX
 DT 13-AUG-1993 (first entry)
 XX
 DE Sequence of apo AI.
 XX
 KW Lipoprotein; apoprotein; B-100; A-I; LDL; HDL; assay.
 XX
 OS Homo sapiens.
 XX
 PN W09307165-A.
 XX
 PD 15-APR-1993.
 XX
 PF 09-OCT-1992; 92WO-US08634.
 XX
 PR 09-OCT-1991; 91US-0774633.
 PR 08-OCT-1992; 92US-0555555.
 PR 28-JUN-1992; 92US-0901706.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Curtiss LK, Koduri KR, Smith RS, Witztum JL, Young SG;
 XX
 DR WPI; 1993-134378/16.
 DR N-PSDB; AAQ40030.
 XX
 PT Polypeptide mimic of native apo B-100 and native apo A-I - useful
 in assays for LDL and HDL in plasma samples
 XX
 PS Claim 19; Pages 105-106; 137pp; English.

CC The inventors claim a portion of the polypeptide contg. apo B-100
 that immunoreacts with antibodies secreted by the hybridoma MB47
 having ATCC Accession No. 8746. Polypeptides specifically claimed
 CC include residues 217-297, 216-310, 216-331, 216-352, 216-377, 1-377,
 CC 205-297, 173-297, 140-297. DNA sequences encoding the polypeptides
 CC are also claimed. Also claimed are a fusion polypeptide that
 CC contains: (a) a first amino acid residue sequence up to 250 residues
 CC in length that includes residues 120-135 of apo A-I, (b) a second
 CC amino acid residue sequence up to 375 residues in length that
 CC includes residues 217-297 of apo B-100 and DNA encoding it.
 XX
 SQ Sequence 267 AA;

Query Match 48.3%; Score 1024; DB 14; Length 267;
 Best Local Similarity 88.5%; Pred. No. 2.5e-60;
 Matches 208; Conservative 6; Mismatches 19; Indels 2; Gaps 1;

QY 180 LEDLRQGLLPVLESFKVSVLSALEEYTKKLNTQGLTKLLDNWDSVTFTSKLRQLGQVPT 239
 DB 35 VADLATVYVDVLKDSGRDYVSQFE--GSAIGKQLNKLKLLDNWDSVTFTSKLRQLGQVPT 92

QY 240 QEFWDNLEKETEGRLQEMSKDLEEVKAKVQPYLDLDFOKKQWQEMELYRQKVEPLRAELQ 299
 DB 93 QEFWDNLEKETEGRLQEMSKDLEEVKAKVQPYLDLDFOKKQWQEMELYRQKVEPLRAELQ 152

QY 300 GARQKLHELOEKLSPGLGEMDRARAHVDALRTHLAPYSDELQRLAARLEALKENGAR 359
 DB 153 GARQKLHELOEKLSPGLGEMDRARAHVDALRTHLAPYSDELQRLAARLEALKENGAR 212

QY 360 LAEYHAKATEHLSTLSEKAKPALEDLROGLLPVLESKVSVLSALEEYTKKLNTQ 414
 DB 213 LAEYHAKATEHLSTLSEKAKPALEDLROGLLPVLESKVSVLSALEEYTKKLNTQ 267

RESULT 5
 AAR72705
 ID AAR72705 standard; Protein; 267 AA.
 XX
 AC AAR72705;
 XX
 DT 31-OCT-1995 (first entry)
 XX
 DE Human apo A-I including signal and propeptide sequences.
 XX
 KW Apo A-I; LDL cholesterol; low density lipoprotein; lipid.
 XX
 OS Homo sapiens.

PH Key Location/Qualifiers
 FT Peptide 1..18
 FT /label= presignal
 FT Peptide 19..24
 FT /label= propeptide
 FT Peptide 120..135
 FT /label= claimed
 FT /note= "as part of fusion polypeptide"
 FT Peptide 19..240
 FT /label= claimed
 FT /note= "as part of fusion polypeptide"

PN US5408038-A.
 XX
 PI 18-APR-1995.
 XX
 PF 09-OCT-1991; 91US-0774633.
 XX
 PR 09-OCT-1991; 91US-0774633.
 PR 18-JUN-1992; 92US-0501706.
 PR 08-OCT-1992; 92US-0959946.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Curtiss LK, Koduri KR, Smith RS, Witztum JL, Young SG;
 XX
 DR WPI; 1995-161146/21.
 DR N-PSDB; AAQ89634.
 XX
 PT New apo:lipoprotein B-100 peptide(s) and fusion peptide(s) - used
 in assay systems for detecting LDL and HDL cholesterol levels in
 PT body fluids.
 XX
 PS Claim 10; Fig 2; 41pp; English.

CC AAA89634 and AAR72705 depict the AA sequence of human apo A-I and its
 corresp. cDNA, including presignal residues and propeptide
 CC residues, according to Seilhamer et al., DNA 3(4):309 (1984).
 CC A dispersible apo A-I/B-100 fusion polypeptide is claimed which
 CC contains a first AA sequence of apo A-I and that includes at
 CC least AA sequence positions 120-135 (see AAR72606) and which reacts
 CC with pan anti-apo AI antibodies such as: AI-4 ATCC HB8744; AI-7
 CC ATCC HB 8745; AI-9 ATCC HB 8741; AI-10 ATCC HB 9200; AI-11 ATCC
 CC HB 9201; AI-12 ATCC HB 9202; AI-13 ATCC HB 9203; AI-14 ATCC HB
 CC 9204; AI-18 ATCC HB 9507.
 XX
 SQ Sequence 267 AA;

Query Match 48.3%; Score 1024; DB 16; Length 267;

Best Local Similarity 88.5%; Pred. No. 2.5e-60;
Matches 208; Conservative 6; Mismatches 19; Indels 2; Gaps 1;

QY 180 LEDLRQGLLPVLSFKVSLSALEEYTKKLTQGTGLKLDNDWSDVTSTFSKLRQGLGPTT 239
Db 35 VKDLATVYVDLVKDSGRDYVSQFE--GSALGKQLNLKLDNDWSDVTSTFSKLRQGLGPTT 92
QY 240 QEFWDNLEKETEGRLQKQMSKDLVEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELQ 299
Db 93 QEFWDNLEKETEGRLQKQMSKDLVEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELQ 152
QY 300 GARQKLHELQKLSPLGEEMRDRARAHVDALRTHLAPYSDELQRLAARLEALKENGAR 359
Db 153 GARQKLHELQKLSPLGEEMRDRARAHVDALRTHLAPYSDELQRLAARLEALKENGAR 212
QY 360 LAEYHAKATEHLSTLSEKAKPALEDLROGLLPVLSFKVSLSALEEYTKKLTQ 414
Db 213 LAEYHAKATEHLSTLSEKAKPALEDLROGLLPVLSFKVSLSALEEYTKKLTQ 267

RESULT 6

AAAY18675
ID AAY18675 standard; Protein; 267 AA.

AC AAY18675;

XX 09-JUL-1999 (first entry)

XX Human apolipoprotein AI protein sequence.

DE Gene therapy; apolipoprotein A-I; agonist; dyslipidemic disorder;
KW ApoA-I; cardiovascular disease; atherosclerosis; restenosis; ICAT;
KW hyperlipidemia; septic shock; lecithin:cholesterol acyltransferase.

XX Homo sapiens.

XX W09916409-A2.

XX 08-APR-1999.

XX 28-SEP-1998; 98WO-US20329.

XX 29-SEP-1997; 97US-0940136.

XX (BUTT/) BUTTNER K.

XX (CORN/) CORNUT I.

XX (DASS/) DASSEUX J.

XX (DUFO/) DUFORCQ J.

XX (METZ/) METZ G.

XX (SEKU/) SEKUL R.

XX Buttner K, Cornut I, Dasseux J, Dufourcq J, Metz G;

XX Sekul R;

XX WPI; 1999-254921/21.

XX N-PSDB; AAX55971.

XX Nucleic acid encoding apolipoprotein A-I agonist peptides

XX Example; Fig 1; 232pp; English.

XX The present invention describes a nucleic acid (A) encoding an
CC apolipoprotein A-I (apoA-I) agonist (B) that is a peptide, or analog,
CC which forms an amphipathic alpha-helix in presence of lipids. (A),
CC optionally as a complex with lipids, and host cells that contain (A),
CC are useful for gene therapy, or prevention, of diseases associated with
CC dyslipidemia, specifically hypercholesterolemia, cardiovascular disease,
CC atherosclerosis, restenosis, HDL (high density lipoprotein) and apoA-I
CC deficiency, hypertriglyceridemia and metabolic syndrome, also to treat
CC endotoxemia (septic shock). Host cells containing (A) can also be used
CC to study the role of apoA-I in lipid metabolism. (B) can be used
CC diagnostically, e.g. to measure serum HDL (particularly its
CC subpopulation involved in retrograde cholesterol transport) and for

CC imaging the circulatory system or HDL accumulations at fatty streaks.
CC The present sequence represents human apoA-I.

SQ Sequence 267 AA;

Query Match 48.3%; Score 1024; DB 20; Length 267;
Best Local Similarity 88.5%; Pred. No. 2.5e-60;
Matches 208; Conservative 6; Mismatches 19; Indels 2; Gaps 1;

QY 180 LEDLRQGLLPVLSFKVSLSALEEYTKKLTQGTGLKLDNDWSDVTSTFSKLRQGLGPTT 239
Db 35 VKDLATVYVDLVKDSGRDYVSQFE--GSALGKQLNLKLDNDWSDVTSTFSKLRQGLGPTT 92
QY 240 QEFWDNLEKETEGRLQKQMSKDLVEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELQ 299
Db 93 QEFWDNLEKETEGRLQKQMSKDLVEVKAKVQPYLDDFQKKWQEEEMELYRQKVEPLRAELQ 152
QY 300 GARQKLHELQKLSPLGEEMRDRARAHVDALRTHLAPYSDELQRLAARLEALKENGAR 359
Db 153 GARQKLHELQKLSPLGEEMRDRARAHVDALRTHLAPYSDELQRLAARLEALKENGAR 212
QY 360 LAEYHAKATEHLSTLSEKAKPALEDLROGLLPVLSFKVSLSALEEYTKKLTQ 414
Db 213 LAEYHAKATEHLSTLSEKAKPALEDLROGLLPVLSFKVSLSALEEYTKKLTQ 267

RESULT 7

AAAB47620
ID AAB47620 standard; Protein; 267 AA.

XX AC AAB47620;

XX 21-JAN-2002 (first entry)

XX Full length Apo-AI.

XX Apolipoprotein; Apo-AI; Apo-A-I fragment T-cell activation inhibitor;
KW AFTI; monocyte; IL-1; interleukin 1; TNF; tumour necrosis factor;
KW acute pancreatitis; Alzheimer's disease; asthma; cancer; fever;
KW inflammatory bowel disease; ischemia; multiple sclerosis; osteoporosis;
KW Parkinson's disease; psoriasis; probe.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Binding-site 44..65

XX /label= Helical lipid binding domain

XX Binding-site 220..241

XX /label= Helical lipid binding domain

XX Domain 74..111

XX /note= "Involved in lipoprotein-mediated cholesterol
efflux from monocytes"

XX Binding-site 149..219

XX /label= Receptor binding domain

XX Domain 99..120

XX /label= Major antigenic epitope domain

XX Domain 99..143

XX /label= Hinged domain

XX Domain 66..120

XX /label= Phylogenetically conserved domain

XX Domain 90..111

XX /note= "Involved in lectin-cholesterol acyltransferase
activity"

XX Domain 44..65

XX /label= Amphipathic helix

XX Domain 66..98

XX /label= Amphipathic helix

XX Domain 99..120

XX /label= Amphipathic helix

XX Domain 121..142

XX /label= Amphipathic helix

XX Domain 143..164

XX /label= Amphipathic helix

FT	Domain	165..208
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FT	/note= "13 kD N-terminal fragment"	
FT	Peptide	136..267
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FT	/note= "13 kD C-terminal fragment"	
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XX		
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Pf	13-MAR-2001; 2001WO-US07826.	
PF		
XX		
PR	13-MAR-2000; 2000US-189008P.	
XX		
XX	(AMGE-) AMGEN INC.	
PA		
XX		
PI	Edwards CK, Burger D, Dayer J, Kohno T;	
PT		
DR	WPI; 2001-596908/57.	
DR	N-PSDB; AAH43623.	
XX		
PT	Apo-A-I fragment T-cell activation inhibitor (AFTI) polynucleotides,	
PT	useful for treating, diagnosing, ameliorating diseases associated with	
PT	IL-1 and/or TNF activity, e.g. acute pancreatitis, Alzheimer's disease	
PT	and asthma .	
XX		
PS	Claim 1; Fig 1A; 132pp; English.	
XX		
CC	This sequence shows full length apolipoprotein (Apo-A1). Fragments	
CC	of Apo-A1 may be used as Apo-A-I fragment T-cell activation inhibitors	
CC	(AFTI). These fragments are selected from an 18 kD N-terminal fragment	
CC	(amino acids 25-194), a 13 kD N-terminal fragment (amino acids 25-144)	
CC	and a 13 kD C-terminal fragment (amino acids 156-267). The AFTI	
CC	polypeptides and polynucleotides are useful for regulating T-cell	
CC	mediated activation of monocytes and for treating, diagnosing,	
CC	ameliorating diseases associated with IL-1 and/or TNF activity.	
CC	The diseases are acute pancreatitis, Alzheimer's disease, asthma,	
CC	cancer, fever, inflammatory bowel disease, ischemia, multiple	
CC	sclerosis, osteoporosis, Parkinson's disease or psoriasis. Numerous	
CC	examples of other diseases are given in the specification.	
CC	The AFTI nucleic acids are useful as hybridization probes in diagnostic	
CC	assays to test for the presence of an AFTI or Apo-A-I DNA in mammalian	
CC	tissue or bodily fluid samples.	
XX		
SQ	Sequence 267 AA;	
	Query Match 48.3%; Score 1024; DB 22; Length 267;	
	Best Local Similarity 88.5%; Pred. No. 2.5e-60;	
	Matches 208; Conservative 6; Mismatches 19; Indels 2; Gaps 1;	
QY	180 LEDRGLLPVLSEKVSFLSALEYTKKLNTQGTLLDNWDVSVTSTFSKUREQLGPVT 239	
	:::: :::: : : :	
Db	35 VKDLAPVVVDVLKSDGRVYSQFE--GSALGKQLNKLNDWNDSVTSTFSKUREQLGPVT 92	
QY	240 QEFWDNLKETEGLRQEMSKDLEEVKAKVPYLDDFOKKWQEEMELYRKVEPLRAELQE 299	
Db	93 QEFWDNLKETEGLRQEMSKDLEEVKAKVPYLDDFOKKWQEEMELYRKVEPLRAELQE 152	
QY	300 GARQKLHELQEKLSPLGEMRDARAHDALRTHLAPSYDELQRLAARLEALKENGAR 359	
Db	153 GARQKLHELQEKLSPLGEMRDARAHDALRTHLAPSYDELQRLAARLEALKENGAR 212	
QY	360 LAEYHAKATEHLUSTSEKAPALDEDLRQGLLPVLSEFKVSFLSALEYTKKLNTQ 414	

CC metabolic defect of apoA-1.
CC Note: this sequence is not given in the specification but is generated
CC from the wild type apoA-1 gene disclosed in the specification and has
CC the appropriate amino acid changed.

Best Local Similarity

Query Match	47.9%;	Score 1014;	DB 15;	Length 264;
Best Local Similarity	81.4%;	Pred. No. 1.1e-59;		
Matches 210;	Conservative 11;	Mismatches 29;	Indels 8	

QY	163	AKATEHLSTLSEKAKP-----ALEDLRQGLLPVLESFKVSFLSALEEYTKKLNTQGTILK	216
DB	9	AVALAGFAITVANADEPPQSPWDRVKDLATVVDVLKDSGRDYSQFE--GSALGKQLNLK	66
QY	217	LLDNWDSVTSTFSKLRLOLGPVTOEFFWNLKEKETEGRLQEMSKDLEEVRAKVQPYLDDFQ	276
DB	67	LLDNWDSVTSTFSKLRLOLGPVTOEFFWNLKEKETEGRLQEMSKDLEEVRAKVQPYLDDFQ	126
QY	277	KWKQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAP	336
DB	127	KWKQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAP	186
QY	337	YSDELQRQLARLALKENGARGARLAETHAKATEHLSLSEKAKPALEDLROGLLPVLESF	396
DB	187	YSDELQRQLARLALKENGARGARLAETHAKATEHLSLSEKAKPALEDLROGLLPVLESF	246
QY	397	KVSFLSALEEYTKKLNTQ 414	
DB	247	RVSFLSALEEYTKKLNTQ 264	
RESULT 11			
ID	AAR56864		
XX	AAR56864 standard; Protein; 264 AA.		
AC	AAR56864;		
DT	26-JAN-1995 (first entry)		
DE	Apo-lipoprotein AI-M.		
KW	Apo-lipoprotein AI-M; Apo AI-M; Escherichia coli; plasmid pKP764;		
KW	vector; atherosclerosis; cardiovascular disease.		
OS	Homo sapiens.		
XX			
PN	W09413819-A.		
PD	23-JUN-1994.		
XX			
PF	09-DEC-1993; 93WO-SR01061.		
XX			
PR	11-DEC-1992; 92SE-0003753.		
XX			
PA	(KABI) KABI PHARMACIA AB.		
XX			
PI	Abrahmsen L, Holmgren E, Kalderen C, Lake M, Mikaelsson A;		
PT	Sejltitz T;		
DR	WPI; 1994-217892/26.		
DR	N-PSDB; AAQ68358.		
XX			
PT	Expression vector for extracellular prodn of apo-lipoprotein AI-M		
PT	in E. coli - Includes inducible promoter and signal peptide		
PT	sequences providing improved yield, useful in treating		
PT	atherosclerosis and cardiovascular disease.		
XX			
PS	Disclosure; Fig. 4; 33pp; English.		
XX			
CC	Plasmid pKP764 encodes human apo-lipoprotein AI-M in E. coli.		
CC	NotI-HindIII segment of pKP764 and the deduced amino acid sequence		
CC	of the translated Apo AI-M protein were determined. The plasmid		
CC	provides high yields of extracellular Apo AI-M.		
XX			
XX	Sequence 264 AA;		
QY	Query Match	47.9%; Score 1014; DB 15; Length 264;	
DB	Best Local Similarity	81.4%; Pred. No. 1.le-59;	
DB	Matches 210; Conservative 11; Mismatches 29; Indels 8; Gaps		
QY	163 AKATEHLSTLSEKAKP-----ALEDLRQGLLPVLESFKVSFLSALEEYTKKLNTQGTILK	216	
DB	9 AVALAGFAITVANADEPPQSPWDRVKDLATVVDVLKDSGRDYSQFE--GSALGKQLNLK	66	


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PD XX 25-OCT-2001.
PF XX 16-APR-2001; 2001WO-US08656.
PR XX 18-APR-2000; 2000US-0552929.
PR XX 26-JAN-2001; 2001US-0770160.
PA (HYSE-) HYSEQ INC.
XX XX
PI Tang YT, Liu C, Drmanac RT;
XX XX WPI; 2001-611725/70.
DR XX
PT Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy.
XX XX
PS Claim 20; Page 199; 765pp; English.
XX XX
CC The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising
CC the nucleic acids encoding the polypeptides and cells genetically
CC engineered to express them are also useful for producing the proteins.
CC The proteins are useful in genetic vaccination, testing and
CC therapy, and can be used as nutritional supplements. They may be used to
CC increase stem cell proliferation; to regulate haematopoiesis; and in
CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
CC immune suppression and/or stimulation; as anti-inflammatory agents; and
CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid
CC sequences of novel human secreted proteins of the invention.
XX XX
SQ Sequence 221 AA;

Query Match 37.2%; Score 788; DB 22; Length 221;
Best Local Similarity 99.4%; Pred. No. 8.3e-45;
Matches 155; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 222 DSVTSTFKLRQLGPGVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFFQKKWQE 281
Db 66 DSVTSTFKLRXLGLGPGVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFFQKKWQE 125
QY 282 EMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEMRDRARAHVDALRTHLAPYSDEL 341
Db 126 EMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEMRDRARAHVDALRTHLAPYSDEL 185
QY 342 RQRLAARLEALKENGARLAEYHAKATEHLSTLSEK 377
Db 186 RQRLAARLEALKENGARLAEYHAKATEHLSTLSEK 221

RESULT 15
AAU30268
ID AAU30268 standard; Protein; 318 AA.
XX AC
XX AC AAU30268;
XX DT
XX DT 18-DEC-2001 (first entry)
XX DE
XX DE Novel human secreted protein #759.
XX KW
XX KW Human; vaccination; gene therapy; nutritional supplement;
XX KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
XX KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX OS
XX OS Homo sapiens.
XX PN
XX PN WO200179449-A2.
XX XX

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PD XX 25-OCT-2001.
XX XX 16-APR-2001; 2001WO-US08656.
XX XX 18-APR-2000; 2000US-0552929.
PR XX 26-JAN-2001; 2001US-0770160.
XX XX (HYSE-) HYSEQ INC.
XX XX
PI Tang YT, Liu C, Drmanac RT;
XX XX WPI; 2001-611725/70.
DR XX
PT Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy.
XX XX
PS Claim 20; Page 270; 765pp; English.
XX XX
CC The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising
CC the nucleic acids encoding the polypeptides and cells genetically
CC engineered to express them are also useful for producing the proteins.
CC The proteins are useful in genetic vaccination, testing and
CC therapy, and can be used as nutritional supplements. They may be used to
CC increase stem cell proliferation; to regulate haematopoiesis; and in
CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
CC immune suppression and/or stimulation; as anti-inflammatory agents; and
CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid
CC sequences of novel human secreted proteins of the invention.
XX XX
SQ Sequence 318 AA;

Query Match 34.3%; Score 726.5; DB 22; Length 318;
Best Local Similarity 76.7%; Pred. No. 1.5e-40;
Matches 161; Conservative 12; Mismatches 28; Indels 9; Gaps 9;

QY 214 TLKLLDNW-DSVTSTFS-KLREOLGPGVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPY 271
Db 84 TLKLLDNWGXSPSTQPSCAKQLGPGVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPY 143
QY 272 -LDDFQKK-WQEEMLYRQKVEPL-RAELQEGAR-QKLHEL-QEKLSPLGEM-RDRARA 325
Db 144 TLDDFQERSWQEEMLYRQKVEPLARKNFQEGARPELSHELARRSLSPGCEAVSRPRAP 203
QY 326 HVDALRTHLAPYSDELQRLA-ARLEALKENGARLAEYHAKATEHLSTLSEKAKPALED 384
Db 204 MWDLRTHLAPYSDEMMPALGRAPICGALRENGGARMGQYHAQTEHLSTLSEKAKPALED 263
QY 385 LROGLLPVLESFKVSFLSALAEYTKKLTQ 414
Db 264 LROGLLPVLESFKVSFLSALAEYTKKLTQ 293

Search completed: April 30, 2003, 15:11:43
Job time : 40 secs

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 30, 2003, 15:11:02 ; Search time 18 Seconds
(without alignments)
676.727 Million cell updates/sec

Title: US-09-990-087-17
Perfect score: 2118
Sequence: 1 MGHHHHIEGRLLDNWD.....SEKVSFLSALEETKRLNTQ 414

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.AA:*
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2: /cgn2.6/ptodata/1/1aa/5B_COMB.pep.*
3: /cgn2.6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2.6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2.6/ptodata/1/1aa/PCTUS_COMB.pep.*
6: /cgn2.6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1024	48.3	267	1 US-07-959-946-3	Sequence 3, Appli
2	1024	48.3	267	1 US-08-333-577-3	Sequence 3, Appli
3	1024	48.3	267	4 US-08-952-796-2	Sequence 2, Appli
4	1024	48.3	267	5 PCT-US92-08634-3	Sequence 3, Appli
5	1017	48.0	264	1 US-08-448-606-6	Sequence 6, Appli
6	1006	47.5	200	4 US-08-952-796-15	Sequence 15, Appli
7	328	15.5	64	2 US-08-292-870-1	Sequence 1, Appli
8	227	10.7	44	2 US-08-292-870-2	Sequence 2, Appli
9	216.5	10.2	366	4 US-09-750-580-3	Sequence 3, Appli
10	198.5	9.4	2101	1 US-08-466-390-4	Sequence 4, Appli
11	198.5	9.4	2101	1 US-08-470-950-4	Sequence 4, Appli
12	198.5	9.4	2101	1 US-08-467-781-4	Sequence 4, Appli
13	198.5	9.4	2101	1 US-08-195-487-4	Sequence 4, Appli
14	198.5	9.4	2101	2 US-08-483-924-4	Sequence 4, Appli
15	198.5	9.4	2101	4 US-09-452-294-1	Sequence 1, Appli
16	198.5	9.4	2101	5 PCT-US93-06160-4	Sequence 4, Appli
17	192.5	9.1	1939	4 US-09-310-187A-1	Sequence 1, Appli
18	191.5	9.0	1886	4 US-08-938-105-3	Sequence 3, Appli
19	190	9.0	534	4 US-09-103-664A-2	Sequence 2, Appli
20	190	9.0	1184	4 US-09-541-782-2	Sequence 2, Appli
21	190	9.0	1184	4 US-09-723-820-2	Sequence 2, Appli
22	185.5	8.8	683	6 5210183-3	Patent No. 5210183
23	183.5	8.7	816	2 US-08-533-306A-6	Sequence 6, Appli
24	183.5	8.7	816	2 US-08-742-923A-6	Sequence 6, Appli
25	183.5	8.7	885	2 US-08-533-306A-4	Sequence 4, Appli
26	183.5	8.7	885	2 US-08-742-923A-4	Sequence 4, Appli
27	183	8.6	477	1 US-08-402-217A-3	Sequence 3, Appli

28	183	8.6	477	1	US-08-700-178-3	Sequence 3, Appli
29	183	8.6	477	3	US-08-995-654-3	Sequence 3, Appli
30	182	8.6	606	4	US-08-477-831C-2	Sequence 2, Appli
31	182	8.6	631	4	US-08-477-831C-11	Sequence 11, Appli
32	181.5	8.6	3248	1	US-08-353-700-1	Sequence 1, Appli
33	181.5	8.6	3248	5	PCT-US95-16216-1	Sequence 1, Appli
34	180.5	8.5	2482	1	US-08-328-254-6	Sequence 6, Appli
35	179.5	8.5	317	4	US-08-949-155-6	Sequence 6, Appli
36	179.5	8.5	317	4	US-09-819-964-6	Sequence 6, Appli
37	175.5	8.3	803	4	US-09-154-750A-85	Sequence 85, Appli
38	175.5	8.3	1068	4	US-09-085-199B-11	Sequence 11, Appli
39	169.5	8.0	515	2	US-08-705-660-46	Sequence 46, Appli
40	169.5	8.0	515	3	US-08-989-045-46	Sequence 46, Appli
41	166	7.8	1588	5	PCT-US93-07261-11	Sequence 11, Appli
42	166	7.8	1663	5	PCT-US93-07261-16	Sequence 16, Appli
43	165	7.8	317	1	US-07-709-949-2	Sequence 2, Appli
44	163.5	7.7	1312	2	US-08-592-126-148	Sequence 148, App
45	163.5	7.7	1312	2	US-08-687-080-51	Sequence 51, Appl

ALIGNMENTS

RESULT 1
US-07-959-946-3
; Sequence 3, Application US/07959946
; Patent No. 5408038
; GENERAL INFORMATION:
; APPLICANT: Smith, Richard K.
; APPLICANT: Koduri, Raju
; APPLICANT: Young, Stephen G.
; APPLICANT: Witzum, Joseph L.
; APPLICANT: Curtiss, Linda K.
; TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
; TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
; ADDRESSEE: Milnamow, Ltd.
; STREET: 180 No. 5408038th Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/959,946
; FILING DATE: 19921008
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,706
; FILING DATE: 18-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Ganson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)616-5400
; TELEFAX: (312)616-5460
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-959-946-3

Query Match 48.3%; Score 1024; DB 1; Length 267;
Best Local Similarity 88.5%; Pred. No. 8.8e-67;
US-07-959-946-3

Db	93	QEFWNLEKTEGLRQMSKDLVEYKAKVOPYLDDFKKQKEEMELYRQKVEPLRAELQE	152
QY	300	GAROKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELQRRLAARLEALKENGAR	359
Db	153	GAROKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELQRRLAARLEALKENGAR	212
QY	360	LAEYHAKATHSLTSLSEKAPPALEDLROGLLPVLESFKVSVLSALEYTKKLNQ	414
Db	213	LAEYHAKATHSLTSLSEKAPPALEDLROGLLPVLESFKVSVLSALEYTKKLNQ	267

RESULT 3
 US-08-952-796-2
 ; Sequence 2, Application US/08952796
 ; Patent No. 6258596
 ; GENERAL INFORMATION:
 ; APPLICANT: BENOIT, Patrick
 ; APPLICANT: BRUCKERT, Eric
 ; APPLICANT: DENEFFE, Patrice
 ; APPLICANT: DUBERGER, Nicolas
 ; APPLICANT: FRUCHART, Jean-Charles
 ; APPLICANT: LUC, Gerald
 ; APPLICANT: TURPIN, Gerrard
 ; APPLICANT: ASSMANN, Gerd
 ; APPLICANT: FUNKE, Harald
 ; TITLE OF INVENTION: NOVEL VARIANTS OF APOLIPOPROTEIN A-I
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Rhone-Poulenc Rorer Inc.
 ; STREET: 500 Arcola Road, Mailstop 3043
 ; CITY: Collegeville
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19426
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/952,796
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: FR 95/06061
 ; FILING DATE: 22-MAY-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO FR96/00747
 ; FILING DATE: 20-MAY-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fehlnert Esq., Paul F.
 ; REGISTRATION NUMBER: 35,135
 ; REFERENCE/DOCKET NUMBER: ST95031-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (610) 454-3839
 ; TELEFAX: (610) 454-3808
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 267 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-952-796-2

	Query Match	48.3%	Score 1024	DB 4	Length 267
	Best Local Similarity	88.5%	Prod. No. 8.e-67		
	Matches 208	Conservative	6	Mismatches 19	Indels 2
	Gaps				
QY	180	LEDLRQGLLPVLESEKVFSLSALEETTKLNTQGTLLKLLDNNDVSTSTFSKLRQLGVPVT	239		
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		::::			
		::::			
DB	35	VKDLATVVDVLDKSGRYDVDFE--GSAIGKQLNLLKLLDNNDVSTSTFSKLRQLGVPVT	92		

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QY 240 QEFWNLKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQE 299
Db 93 QEFWNLKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQE 152
QY 300 GARQKLHELQEKLSPLGEEMDRARAHVDALRTHLAPYSDELQRLAARLEALKENGAR 359
Db 153 GARQKLHELQEKLSPLGEEMDRARAHVDALRTHLAPYSDELQRLAARLEALKENGAR 212
QY 360 LAEYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALEEYTKKLNQ 414
Db 213 LAEYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALEEYTKKLNQ 267

RESULT 4
PCT-US92-08634-3
; Sequence 3, Application PC/TUS9208634
; GENERAL INFORMATION:
; APPLICANT: Smith, Richard K.
; APPLICANT: Koduri, Raju
; APPLICANT: Young, Stephen G.
; APPLICANT: Witztum, Joseph L.
; APPLICANT: Curtiss, Linda K.
; TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
; TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore, Sukter &
; ADDRESSEE: Milnamow, Ltd.
; STREET: 180 North Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/08634
; FILING DATE: 19921009
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,706
; FILING DATE: 18-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)616-5400
; TELEFAX: (312)616-5460
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US92-08634-3

Query Match 48.3%; Score 1024; DB 5; Length 267;
Best Local Similarity 88.5%; Pred. No. 8.8e-67;
Matches 208; Conservative 6; Mismatches 19; Indels 2; Gaps 1;

QY 180 LEDLRQGLLPVLESFKVSFLSALEEYTKKLNQGTGLKLDNWDVSTFSKLRQGLGPT 239
Db 35 VKDLATVYDVLDKSGRDYVSQFE--GSALGKQLNLKLDNWDVSTFSKLRQGLGPT 92
QY 240 QEFWNLKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQE 299
Db 93 QEFWNLKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQE 152
QY 300 GARQKLHELQEKLSPLGEEMDRARAHVDALRTHLAPYSDELQRLAARLEALKENGAR 359
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Db 153 GARQKLHELQEKLSPLGEEMDRARAHVDALRTHLAPYSDELQRLAARLEALKENGAR 212
QY 360 LAEYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALEEYTKKLNQ 414
Db 213 LAEYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALEEYTKKLNQ 267

RESULT 5
US-08-448-606-6
; Sequence 6, Application US/08448606
; Patent No. 5721114
; GENERAL INFORMATION:
; APPLICANT: Abrahams n, Lars
; APPLICANT: Holmgren, Erik
; APPLICANT: Kalder n, Christina
; APPLICANT: Lake, Mats
; APPLICANT: Mikaelsson, sa
; APPLICANT: Sejlitz, Torsten
; TITLE OF INVENTION: Expression System For Producing
; TITLE OF INVENTION: Apolipoprotein AI-M
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pollock, Vande Sande & Priddy
; STREET: 1990 M Street, N.W., Suite 800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,606
; FILING DATE: 25-AUG-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/SE93/01061
; FILING DATE: 09-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9203753-0
; FILING DATE: 11-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Amernick, Burton A.
; REGISTRATION NUMBER: 24,852
; REFERENCE/DOCKET NUMBER: 0151/00121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)331-7111
; TELEFAX: (202) 293-6229
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 264 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-448-606-6

Query Match 48.0%; Score 1017; DB 1; Length 264;
Best Local Similarity 81.8%; Pred. No. 2.8e-66;
Matches 211; Conservative 10; Mismatches 29; Indels 8; Gaps 2;

QY 163 AKATEHLSTLSEKAKP-----ALEDLRQGLLPVLESFKVSFLSALEEYTKKLNQGTGLK 216
Db 9 AVALAGFATVANADPPSPWDRVKDLATVYVDVLKDSGRDYSQFE--GSALGKQLNLK 66
QY 217 LLDNWDVSTFSKLRQGLGPTQEFWNLKETEGLRQEMSKDLEEVKAKVQPYLDDFQ 276
Db 67 LLDNWDVSTFSKLRQGLGPTQEFWNLKETEGLRQEMSKDLEEVKAKVQPYLDDFQ 126
QY 277 KKWQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGEEMDRARAHVDALRTHLAP 336
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Db 127 KKQWEEMLYRQKVEPLRAELQEGARQKLHELQEKLSPLGEMRDRARAHVDALRTHLAP 186
QY 337 YSELRORLAARLEALKENGARLAHYHAKATEHLSTLSEKAKPALEDLROGLLPVLESF 396
Db 187 YSELROCLAARLEALKENGARLAHYHAKATEHLSTLSEKAKPALEDLROGLLPVLESF 246
QY 397 KVSFLSALEEYTKKLNQ 414
Db 247 KVSFLSALEEYTKKLNQ 264
RESULT 6
US-08-952-796-15
; Sequence 15, Application US/08952796
; Patent No. 6258596
; GENERAL INFORMATION:
; APPLICANT: BENOIT, Patrick
; APPLICANT: BRUCKERT, Eric
; APPLICANT: DENEFLÉ, Patrice
; APPLICANT: DUBERGER, Nicolas
; APPLICANT: FRUCHART, Jean-Charles
; APPLICANT: LUC, Gerald
; APPLICANT: TURPIN, Gerard
; APPLICANT: ASSMANN, Gerd
; APPLICANT: FUNKE, Harald
; TITLE OF INVENTION: NOVEL VARIANTS OF APOLIPOPROTEIN A-I
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mailstop 3c43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/952,796
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95/06061
; FILING DATE: 22-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO FR96/00747
; FILING DATE: 20-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Fehlnér Esq., Paul F.
; REGISTRATION NUMBER: 35,135
; REFERENCE/DOCKET NUMBER: ST95031-US
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 200 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-952-796-15
Query Match 47.5%; Score 1006; DB 4; Length 200;
Best Local Similarity 99.5%; Pred. No. 1.2e-65;
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 215 LKLLDNWDSVTSTFSKLEQGLPVTQEFWDNLEKETEGRLQEMSKDLFEVAKVQPYLDD 274
Db 1 LKLLDNWDSVTSTFSKLEQGLPVTQEFWDNLEKETEGRLQEMSKDLFEVAKVQPYLDD 60
QY 275 FOKKQWEEMLYRQKVEPLRAELQEGARQKLHELQEKLSPLGEMRDRARAHVDALRTHL 334

Db 61 FOKKQWEEMLYRQKVEPLRAELQEGARQKLHELQEKLSPLGEMRDRARAHVDALRTHL 120
QY 335 APYSELQRLAARLEALKENGARLAHYHAKATEHLSTLSEKAKPALEDLROGLLPVLE 394
Db 121 APYSELQRLAARLEALKENGARLAHYHAKATEHLSTLSEKAKPALEDLROGLLPVLE 180
QY 395 SFKVSFLSALEEYTKKLNQ 414
Db 181 SFKVSFLSALEEYTKKLNQ 200
RESULT 7
US-08-292-870-1
; Sequence 1, Application US/08292870
; Patent No. 5814467
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Linda K
; APPLICANT: Banka, Carole L
; APPLICANT: Bonnet, David J
; APPLICANT: Smith, Richard S
; TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS
; TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESS: Patent Counsel
; STREET: 10666 No. 581467th Torrey Pines Road., TPC 8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,870
; FILING DATE: 17-AUG-1994
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/534,761
; FILING DATE: 07-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/711,333
; FILING DATE: 06-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US 91/04038
; FILING DATE: 07-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 210.1 D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 64 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-292-870-1
Query Match 15.5%; Score 328; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 2.2e-17;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 256 EMSKDLFEVAKVQPYLDDFQKKQWEEMLYRQKVEPLRAELQEGARQKLHELQEKLSPL 315

;; TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
;; NUMBER OF SEQUENCES: 6
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
;; STREET: 125 HIGH STREET
;; CITY: BOSTON
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02110
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/466,390
;; FILING DATE: 06-JUN-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: PITCHER ESO, EDMUND R
;; REGISTRATION NUMBER: 27,829
;; REFERENCE/DOCKET NUMBER: MTP-013
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 248-7000
;; TELEFAX: (617) 248-7100
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2101 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-466-390-4

Query Match 9.4%; Score 198.5; DB 1; Length 2101;
Best Local Similarity 24.7%; Pred. No. 3e-06;
Matches 95; Conservative 67; Mismatches 139; Indels 83; Gaps 16;
QY 27 SKLRQLGPVTQEFWNLNLEKETEGRLQEMSKDLE-----EVKAKVQPYLDDFQKK 76
Db 594 ASLRR-----DAALKQLEALEKEKAKEILQOQLQVANEARDSAQTSVTAQR- 643
QY 77 WOEMELYRQKVEPLRAELQEGARQKHELOEKLSPLGEMRDRARAHVDALRTHLAPYS 136
Db 644 --EKALSR-KVEELQA-CVETARQEQHEAQAQVALEQLRSEQQKATE--KERVAQEK 697
QY 137 DELRQRLAARLEALKENGARLAHYHAKATEHLSTLSEKAKPALEDLROGLLPVLESEKV 196
Db 698 DLQLOQLQALKESLKVTKGS-LEEKKRAADAL-----EEQRCISELKAETRSLEQHKR 752
QY 197 SFLSALEEYTKLNTQGTLLKLDNWDVSTFSLRQLGPVTQEFWNLNLEKETEGRLQ 256
b 753 ERKELEERAGRKGLEARLL-----QLGEAHQ-----AETEVLRR 788
QY 257 MSK-----DLEEVKAKVQPYLDDFQKKWQEME---LYRQKVEPLRAELQEGARQ 303
Db 789 LAEAMAAQHTAESECEQLVKEVAWRDGYEDSQEEAQYGAMFQQLMTLKEEC-ERAKQ 847
QY 304 KLHELOEKLS-----PLGEMRDRARAHVDALRTHLAPYSDELQ-ORLAARLEALKE 354
Db 848 ELQEAKEKVAGIESHSELQISROQNKLAELHANLARALQOQVEKVRQAQKLADDLSTLQ 907
QY 355 NGGARLAHYHAKATEHLSTLSEKA 378
Db 908 KMAAT-----SKEVARLETLLVRKA 926

RESULT 11
US-08-470-950-4
; Sequence 4, Application US/08470950
; Patent No. 5698439
; GENERAL INFORMATION:
; APPLICANT: TOUKATLY, GARY
; APPLICANT: LIDGARD, GRAHAM P

;; TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
;; TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
;; NUMBER OF SEQUENCES: 6
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
;; STREET: 125 HIGH STREET
;; CITY: BOSTON
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02110
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/470,950
;; FILING DATE: 06-JUN-1995
;; CLASSIFICATION: 536
;; ATTORNEY/AGENT INFORMATION:
;; NAME: PITCHER ESO, EDMUND R
;; REGISTRATION NUMBER: 27,829
;; REFERENCE/DOCKET NUMBER: MTP-013
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 248-7000
;; TELEFAX: (617) 248-7100
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2101 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-470-950-4

Query Match 9.4%; Score 198.5; DB 1; Length 2101;
Best Local Similarity 24.7%; Pred. No. 3e-06;
Matches 95; Conservative 67; Mismatches 139; Indels 83; Gaps 16;
QY 27 SKLRQLGPVTQEFWNLNLEKETEGRLQEMSKDLE-----EVKAKVQPYLDDFQKK 76
Db 594 ASLRR-----DAALKQLEALEKEKAKEILQOQLQVANEARDSAQTSVTAQR- 643
QY 77 WOEMELYRQKVEPLRAELQEGARQKHELOEKLSPLGEMRDRARAHVDALRTHLAPYS 136
Db 644 --EKALSR-KVEELQA-CVETARQEQHEAQAQVALEQLRSEQQKATE--KERVAQEK 697
QY 137 DELRQRLAARLEALKENGARLAHYHAKATEHLSTLSEKAKPALEDLROGLLPVLESEKV 196
Db 698 DLQLOQLQALKESLKVTKGS-LEEKKRAADAL-----EEQRCISELKAETRSLEQHKR 752
QY 197 SFLSALEEYTKLNTQGTLLKLDNWDVSTFSLRQLGPVTQEFWNLNLEKETEGRLQ 256
Db 753 ERKELEERAGRKGLEARLL-----QLGEAHQ-----AETEVLRR 788
QY 257 MSK-----DLEEVKAKVQPYLDDFQKKWQEME---LYRQKVEPLRAELQEGARQ 303
Db 789 LAEAMAAQHTAESECEQLVKEVAWRDGYEDSQEEAQYGAMFQQLMTLKEEC-ERAKQ 847
QY 304 KLHELOEKLS-----PLGEMRDRARAHVDALRTHLAPYSDELQ-ORLAARLEALKE 354
Db 848 ELQEAKEKVAGIESHSELQISROQNKLAELHANLARALQOQVEKVRQAQKLADDLSTLQ 907
QY 355 NGGARLAHYHAKATEHLSTLSEKA 378
Db 908 KMAAT-----SKEVARLETLLVRKA 926

RESULT 12
US-08-467-781-4
; Sequence 4, Application US/08467781
; Patent No. 5780596
; GENERAL INFORMATION:
; APPLICANT: TOUKATLY, GARY

APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 125 HIGH STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,781
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2101 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-467-781-4

Query Match 9.4%; Score 198.5; DB 1; Length 2101;
Best Local Similarity 24.7%; Pred. No. 3e-06;
Matches 95; Conservative 67; Mismatches 139; Indels 83; Gaps 16;

QY 27 SKLRQLGPTQEFWDNLEKETGLRQEMSKDLE-----EVKAKVPYLDLDFQKK 76
Db 594 ASLSR-----DAALKQLEALEKEKALEILQQLQVANEARDSAQTSVTOAQR- 643

QY 77 WOEMEELRYOKVPEPLRAELQEGARQKLHELOEKLSPLEEMRDRARAHVDALRTHLAPYS 136
Db 644 --EKAELSR-KVEELQA-CVETARQEQHEAQVAELEQLRSEQQKATE--KERVQAEK 697

QY 137 DELRQRLAARLEALKENGARLAHYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKV 196
Db 698 DLQEQQLQALKESLKVTKGS-LEEEKRAADAL-----EEQRCISSELKAEATRSILVEQHKR 752

QY 197 SFLSALAEYTKKLTNGTGLKLLDNWDSVTSTFSKLRLQGLPVTQEFWDNLEKETGLROE 256
Db 753 ERKELEERAGRGKLEARLL-----OLGEAHQ-----AETEVLRR 788

QY 257 MSK-----DLEEVKAKVPYLDLDFQKKQWEME---LYRKVPEPLRAELQEGARQ 303
Db 789 LAEAMAAQHTAESECEQLVKEVAARWDGYEDSQEQEAQYGAMFOQLMTLKEEC-EKARQ 847

QY 304 KLHELOEKL-----PLGEMRDRARAHVDALRTHLAPYSDELRLQRLAARLEALKE 354
Db 848 ELQEAKEKVGAGIESHSELQISROONKLAELHANLARALQVQKEKVRQAQLADLSTLQ 907

QY 355 NGGARLAHYHAKATEHLSTLSEKA 378
Db 908 KMAAT-----SKEVARLETIVRKA 926

RESULT 13
US-08-195-487-4
; Sequence 4, Application US/08195487
; Patent No. 5783403
; GENERAL INFORMATION:

APPLICANT: TOUKATLY, GARY
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA HURWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,487
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/901,701
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2101 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-195-487-4

Query Match 9.4%; Score 198.5; DB 1; Length 2101;
Best Local Similarity 24.7%; Pred. No. 3e-06;
Matches 95; Conservative 67; Mismatches 139; Indels 83; Gaps 16;

QY 27 SKLRQLGPTQEFWDNLEKETGLRQEMSKDLE-----EVKAKVPYLDLDFQKK 76
Db 594 ASLSR-----DAALKQLEALEKEKALEILQQLQVANEARDSAQTSVTOAQR- 643

QY 77 WOEMEELRYOKVPEPLRAELQEGARQKLHELOEKLSPLEEMRDRARAHVDALRTHLAPYS 136
Db 644 --EKAELSR-KVEELQA-CVETARQEQHEAQVAELEQLRSEQQKATE--KERVQAEK 697

QY 137 DELRQRLAARLEALKENGARLAHYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKV 196
Db 698 DLQEQQLQALKESLKVTKGS-LEEEKRAADAL-----EEQRCISSELKAEATRSILVEQHKR 752

QY 197 SFLSALAEYTKKLTNGTGLKLLDNWDSVTSTFSKLRLQGLPVTQEFWDNLEKETGLROE 256
Db 753 ERKELEERAGRGKLEARLL-----OLGEAHQ-----AETEVLRR 788

QY 257 MSK-----DLEEVKAKVPYLDLDFQKKQWEME---LYRKVPEPLRAELQEGARQ 303
Db 789 LAEAMAAQHTAESECEQLVKEVAARWDGYEDSQEQEAQYGAMFOQLMTLKEEC-EKARQ 847

QY 304 KLHELOEKL-----PLGEMRDRARAHVDALRTHLAPYSDELRLQRLAARLEALKE 354
Db 848 ELQEAKEKVGAGIESHSELQISROONKLAELHANLARALQVQKEKVRQAQLADLSTLQ 907

QY 355 NGGARLAHYHAKATEHLSTLSEKA 378
Db 908 KMAAT-----SKEVARLETIVRKA 926

RESULT 14

US-08-483-924-4
; Sequence 4, Application US/08483924
; Patent No. 5882876
; GENERAL INFORMATION:
; APPLICANT: TOURATLY, GARY
; APPLICANT: LIDGARD, GRAHAM P
; TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
; TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,924
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESO, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: MTP-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2101 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-924-4

Query Match 9.4%; Score 198.5; DB 2; Length 2101;
Best Local Similarity 24.7%; Pred. No. 3e-06;
Matches 95; Conservative 67; Mismatches 139; Indels 83; Gaps 16;
QY 27 SKLREQLGVPVTFQFWDNLEKETEGLRQEMSKDLE-----EVKAKVQVPYLDLDDFOKK 76
Db 594 ASLSR-----DAALKQLEALEKEKALEILQOQLQVANEARDSAQTSVTQAQR- 643
QY 77 WQEMELYRQKVEPLRAELQEGAROKLHELQEKLSPLGEMRDRARAHVDALRTHLAPYS 136
Db 644 --EKAELSR-KVEELQA-CVETARQEQHEAQAQVAELELQRLSEQQKATE--KERVAQEK 697
QY 137 DELRQRLAARLEALKENGARLAHEYHAKATEHLSTLSEKAKPALEDRLQGLLPVLESFKV 196
Db 698 DQLEQQLQALKESLKVTKGS-LEEKKRAADAL---BEQRCISELKAETRSVLVQHKR 752
QY 197 SFLSALAEYTKKLTQGTGLKLDNWDVSTFTSKLREQLGVPVTFQFWDNLEKETEGLRQE 256
Db 753 ERKLEEEERAGRKGLEARLL-----QLGEAHQ-----AETEVLRRE 788
QY 257 MSK-----DLEEVKAKVQPYLDLDDFOKKWQEME---LYRQKVEPLRAELQEGARQ 303
Db 789 LAEAMAAQHTAESECEQLVKEVAAWRDGYDSQEQEAQYGAMFQQLMTLKEEC-EKARQ 847
QY 304 KLHELQEKLS-----PLGEMRDRARAHVDALRTHLAPYSDELRL-ORLAARLEALKE 354
Db 848 ELQEAKEKVAGIESHSELQISROQNKLAELHANLARALQOQVEKVRQAQKLADDLSTLQE 907
QY 355 NGGARLAHEYHAKATEHLSTLSEKA 378
Db 908 KMAAT-----SKEVARLETILVRKA 926

Search completed: April 30, 2003, 15:14:33
Job time : 23 secs

RESULT 15
US-09-452-294-1
; Sequence 1, Application US/09452294
; Patent No. 6287790
; GENERAL INFORMATION:
; APPLICANT: Lelievre, Sophie
; APPLICANT: Bissell, Mina
; TITLE OF INVENTION: UTILIZATION OF NUCLEAR STRUCTURAL PROTEINS FOR TARGETED
; TITLE OF INVENTION: THERAPY AND DETECTION OF PROLIFERATIVE AND
; TITLE OF INVENTION: DIFFERENTIATION DISORDERS
; FILE REFERENCE: IB-1454- Sequence Submittal
; Patent No. 6287790
; CURRENT APPLICATION NUMBER: US/09/452,294
; CURRENT FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/110,420
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-452-294-1
Query Match 9.4%; Score 198.5; DB 4; Length 2101;
Best Local Similarity 24.7%; Pred. No. 3e-06;
Matches 95; Conservative 67; Mismatches 139; Indels 83; Gaps 16;
QY 27 SKLREQLGVPVTFQFWDNLEKETEGLRQEMSKDLE-----EVKAKVQVPYLDLDDFOKK 76
Db 594 ASLSR-----DAALKQLEALEKEKALEILQOQLQVANEARDSAQTSVTQAQR- 643
QY 77 WQEMELYRQKVEPLRAELQEGAROKLHELQEKLSPLGEMRDRARAHVDALRTHLAPYS 136
Db 644 --EKAELSR-KVEELQA-CVETARQEQHEAQAQVAELELQRLSEQQKATE--KERVAQEK 697
QY 137 DELRQRLAARLEALKENGARLAHEYHAKATEHLSTLSEKAKPALEDRLQGLLPVLESFKV 196
Db 698 DQLEQQLQALKESLKVTKGS-LEEKKRAADAL---EEQRCISELKAETRSVLVQHKR 752
QY 197 SFLSALAEYTKKLTQGTGLKLDNWDVSTFTSKLREQLGVPVTFQFWDNLEKETEGLRQE 256
Db 753 ERKLEEEERAGRKGLEARLL-----QLGEAHQ-----AETEVLRRE 788
QY 257 MSK-----DLEEVKAKVQPYLDLDDFOKKWQEME---LYRQKVEPLRAELQEGARQ 303
Db 789 LAEAMAAQHTAESECEQLVKEVAAWRDGYDSQEQEAQYGAMFQQLMTLKEEC-EKARQ 847
QY 304 KLHELQEKLS-----PLGEMRDRARAHVDALRTHLAPYSDELRL-ORLAARLEALKE 354
Db 848 ELQEAKEKVAGIESHSELQISROQNKLAELHANLARALQOQVEKVRQAQKLADDLSTLQE 907
QY 355 NGGARLAHEYHAKATEHLSTLSEKA 378
Db 908 KMAAT-----SKEVARLETILVRKA 926

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 30, 2003, 15:13:43 ; Search time 47 Seconds
(without alignments)
760.057 Million cell updates/sec

Title: US-09-990-087-17

Perfect score: 2118

Sequence: 1 MGHSHHHHIEGRKLNDWD.....SFKVSFSLAEETKTLNTQ 414

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328255 seqs, 86286685 residues

Total number of hits satisfying chosen parameters: 328255

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pap.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pap.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pap.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pap.*
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12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pap.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pap.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1065	50.3	336	9	US-09-987-107-44
2	1063.5	50.2	337	9	US-09-987-107-46
3	1057	49.9	324	9	US-09-987-107-62
4	1056	49.9	316	9	US-09-987-107-48
5	1056	49.9	324	9	US-09-987-107-64
6	1051	49.6	316	9	US-09-987-107-54
7	1051	49.6	324	9	US-09-987-107-66
8	1049.5	49.6	323	9	US-09-987-107-58
9	1047.5	49.5	323	9	US-09-987-107-56
10	1045.5	49.4	323	9	US-09-987-107-60
11	1042	49.2	304	9	US-09-987-107-8
12	1041	49.2	304	9	US-09-987-107-7
13	1039.5	49.1	261	9	US-09-987-107-52
14	1038	49.0	304	9	US-09-987-107-6
15	1036.5	48.9	301	9	US-09-987-107-5
16	1036	48.9	306	9	US-09-987-107-9
17	1035.5	48.9	301	9	US-09-987-107-3
18	1034	48.8	306	9	US-09-987-107-11
19	1034	48.8	344	9	US-09-987-107-68

20	1033	48.8	306	9	US-09-987-107-10
21	1031.5	48.7	273	9	US-09-987-107-50
22	1029	48.6	258	9	US-09-987-107-4
23	1024	48.3	243	9	US-09-987-107-1
24	1024	48.3	244	9	US-09-987-107-2
25	1024	48.3	267	9	US-09-987-107-15
26	1024	48.3	267	9	US-09-802-640-30
27	1024	48.3	267	10	US-09-803-918A-2
28	1024	48.3	329	9	US-09-987-107-14
29	991.5	46.8	266	9	US-09-987-107-16
30	860.5	40.6	266	9	US-09-987-107-19
31	837	39.5	266	9	US-09-987-107-20
32	814	38.4	265	9	US-09-987-107-18
33	798	37.7	265	9	US-09-987-107-17
34	701.5	33.1	265	9	US-09-987-107-21
35	668	31.5	170	10	US-09-803-918A-3
36	653	30.8	264	9	US-09-987-107-22
37	614	29.0	241	9	US-09-987-107-24
38	584	27.6	259	9	US-09-987-107-23
39	505.5	23.9	264	9	US-09-987-107-27
40	491.5	23.2	264	9	US-09-987-107-25
41	470.5	22.2	264	9	US-09-987-107-26
42	350.5	16.5	429	9	US-09-987-107-34
43	339.5	16.0	401	9	US-09-987-107-36
44	324.5	15.3	396	10	US-09-800-729-207
45	320.5	15.1	396	9	US-09-987-107-33

ALIGNMENTS

RESULT 1
US-09-987-107-44
; Sequence 44, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT FILING DATE: 2001-11-13
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patent version 3.1
; SEQ ID NO 44
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pT7 H6ubiF Apo A-1 plasmid
US-09-987-107-44
Query Match 50.3%; Score 1065; DB 9; Length 336;
Best Local Similarity 57.7%; Pred. No. 2.8e-53;
Matches 240; Conservative 27; Mismatches 67; Indels 82; Gaps 7;
QY 1 MGHSHHHHIEGRKLNDWDNSTVTSFKLREQLPVTOEFWNLKEFTEGLRQEMSKDLE 60
Db 1 MGHSHHHH-HG-----SQIFVTKLTGKTITLEVEPDSRTIE 34
QY 61 EVKAKYQPYLDDFQKKWOQEMELYRQKVEPLRAELQEGAROKLHELOEKLSPGGEEMDR 120
Db 35 NVKAKIQD-----KCIIPDQQRLLIFAGKQLEDGRTLSDYNIQ-KESTLHLVLKLR 84
QY 121 ARAHVDALETHLAPYS--DELQRQLAARLEALKENGARLAIEYHAKATEHLSTLSEKAKP 178
Db 85 G-GSIEGRGGDEFPQSPWDRVKDLATVYVDLKDGRDVSQFEGSA----- 130

Qy 179 ALEDROGLLPVLESFKVSVFLSALAEYTKKLNQGTGLKLLDNWDSVTSTFSKLRQLGVPV 238
Db 131 -----LGKQLNLKLLDNWDSVTSTFSKLRQLGVPV 160
Qy 239 TQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQ 298
Db 161 TQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQ 220
Qy 299 EGARQKHELOEKLSPGEMRDRARAHVDALRTHLAPYSDELQRRLAARLEAKENGGA 358
Db 221 EGARQKHELOEKLSPGEMRDRARAHVDALRTHLAPYSDELQRRLAARLEAKENGGA 280
Qy 359 RLAEYHAKATEHLSTSEKAKPALEDROGLLPVLESFKVSVFLSALAEYTKKLNQ 414
Db 281 RLAEYHAKATEHLSTSEKAKPALEDROGLLPVLESFKVSVFLSALAEYTKKLNQ 336

RESULT 2
US-09-987-107-46
; Sequence 46, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T7 H6b1fx Cys-Apo A-1 plasmid
US-09-987-107-46

Query Match 50.2%; Score 1063.5; DB 9; Length 337;
Best Local Similarity 57.5%; Pred. No. 3.4e-53;
Matches 242; Conservative 25; Mismatches 63; Indels 91; Gaps 8;

Qy 1 MGHSHHHH-HG-----SQIFVKTLTGKTTITLEVEPSDTIE 34
Db 1 MGHSHHHH-HG-----SQIFVKTLTGKTTITLEVEPSDTIE 34
Qy 61 EVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKHELOEKLSPGEMRDR 120
Db 35 NVKAKIOD-----KEGIPPDQQLIFAGKQLEDGRTLSYNIQ-KESTLHLVLRLR 84
Qy 121 -----ARAHVDALRTHLAPYS--DELQRRLAARLEAKENGARLAAYHAKATEHLSTLS 173
Db 85 GSGTEGRGCCDE-----PPQSPWDRVKDLATVYVDLVKDSGRDYVSQFEGSA ----- 131
Qy 174 EKAKPALEDROGLLPVLESFKVSVFLSALAEYTKKLNQGTGLKLLDNWDSVTSTFSKLR 233
Db 132 -----LGKQLNLKLLDNWDSVTSTFSKLR 156
Qy 234 QLGPVPTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPL 293
Db 157 QLGPVPTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPL 216
Qy 294 RAELOEGARQKHELOEKLSPGEMRDRARAHVDALRTHLAPYSDELQRRLAARLEAK 353
Db 217 RAELOEGARQKHELOEKLSPGEMRDRARAHVDALRTHLAPYSDELQRRLAARLEAK 276

Qy 354 ENGARLAAYHAKATEHLSTSEKAKPALEDROGLLPVLESFKVSVFLSALAEYTKKLN 413
Db 277 ENGARLAAYHAKATEHLSTSEKAKPALEDROGLLPVLESFKVSVFLSALAEYTKKLN 336
Qy 414 Q 414
Db 337 Q 337

RESULT 3
US-09-987-107-62
; Sequence 62, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pT7H6 (GS)3 Trip-A-Tn-Apo A1 AmpR plasmid
US-09-987-107-62

Query Match 49.9%; Score 1057; DB 9; Length 324;
Best Local Similarity 56.3%; Pred. No. 7.6e-53;
Matches 238; Conservative 33; Mismatches 44; Indels 108; Gaps 11;

Qy 1 MGHSHHHH-----IEGRKLKLLDNWDSVTSTFSKLRQLGVPVTOEFWDNLEKETEGLRQ 53
Db 1 MGHSHHHHGGSGSIQGRSPGTE-----PPTQK-----PKKIVNAKK 38
Qy 54 EM--SKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKHELOEKL 111
Db 39 DVVNTKMFELKSR-----LDTL---AQEVALLEKQ-QALQTVSLKGS--KVHMKPEPPQS 87
Qy 112 PLGEMRDRARAHVDALRTHLAPYSDELQRRLAARLEAKENGARLAAYHAKATEHLST 171
Db 88 P-WDRVKDLATVYVD-----VLKDSGRDYVSQFEGSA----- 118
Qy 172 LSEKAKPALEDROGLLPVLESFKVSVFLSALAEYTKKLNQGTGLKLLDNWDSVTSTFSKL 231
Db 119 -----LGKQLNLKLLDNWDSVTSTFSKL 141
Qy 232 RQLGVPVTOEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVE 291
Db 142 RQLGVPVTOEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVE 201
Qy 292 PLRAELOEGARQKHELOEKLSPGEMRDRARAHVDALRTHLAPYSDELQRRLAARLEA 351
Db 202 PLRAELOEGARQKHELOEKLSPGEMRDRARAHVDALRTHLAPYSDELQRRLAARLEA 261
Qy 352 LKENGARLAAYHAKATEHLSTSEKAKPALEDROGLLPVLESFKVSVFLSALAEYTKKL 411
Db 262 LKENGARLAAYHAKATEHLSTSEKAKPALEDROGLLPVLESFKVSVFLSALAEYTKKL 321
Qy 412 NTQ 414
Db 322 NTQ 324

RESULT 4
US-09-987-107-48
; Sequence 48, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987.107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR FILING DATE: 2001-01-26
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pT7 H6 Trip-A-Apo A-1 - AmpR plasmid
US-09-987-107-48

Query Match 49.98; Score 1056; DB 9; Length 316;
Best Local Similarity 54.48; Pred. No. 8.4e-53;
Matches 234; Conservative 25; Mismatches 41; Indels 130; Gaps 8;
QY 1 MGHHHHH---IEGR-----LKLLDNWDSVTST--FSLRQLGVPVQEFWDL 44
DB 1 MGSHHHHHSGISQGRSPCTEPTQPKKIVNAKDVNTKMFELKSR-----DTL 52
QY 45 EKETEGLRQEMSKDLEEVKAKVQPYLDDFOKKWQEMELYRQKVEPLRAELQEGAROKLH 104
DB 53 AQEALLKEQALQTVSLKGSDEPP---QSPW-----VLKDSGRDVSQFEGS 81
QY 105 ELQEKLSPLGEMDRARAHVDALRTHLAPYSDELQRLAARLEAKENGARGARLAHYHAK 164
DB 82 -----DRVKDLATVYD-----VLKDSGRDVSQFEGS 109
QY 165 ATEHLSTSEKAKPALEDLROGLLPVLESFKVFSLSALEEYTKKLTQGTCLKLLDNWDSV 224
DB 110 A-----LQKLNKLLDNWDSV 126
QY 225 TSFSLRQLGVPVQEFWDLNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFOKKWQEME 284
DB 127 TSFSLRQLGVPVQEFWDLNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFOKKWQEME 186
QY 285 LYRQKVEPLRAELQEGAROKLHELOEKLSPLGEMDRARAHVDALRTHLAPYSDELQRL 344
DB 187 LYRQKVEPLRAELQEGAROKLHELOEKLSPLGEMDRARAHVDALRTHLAPYSDELQRL 246
QY 345 LAARLEAKENGARGARLAHYHAKATEHLSTSEKAKPALEDLROGLLPVLESFKVFSLSAL 404
DB 247 LAARLEAKENGARGARLAHYHAKATEHLSTSEKAKPALEDLROGLLPVLESFKVFSLSAL 306
QY 405 EYTKKLTQ 414
DB 307 EYTKKLTQ 316

RESULT 5
US-09-987-107-64
; Sequence 64, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA

; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pT7H6 Trip-A-Tn-Apo A1-final - AmpR plasmid
US-09-987-107-64

Query Match 49.98; Score 1056; DB 9; Length 324;
Best Local Similarity 56.38; Pred. No. 8.6e-53;
Matches 238; Conservative 32; Mismatches 45; Indels 108; Gaps 11;
QY 1 MGHHHHH-----TEGRKLKLLDNWDSVTSTFSLRQLGVPVQEFWDLNLEKETEGLRQ 53
DB 1 MGSHHHHHSGISQGRSPGTE-----PPTQK-----PKKIVNAKK 38
QY 54 EM--SKDLEEVKAKVQPYLDDFOKKWQEMELYRQKVEPLRAELQEGAROKLHELOEKLS 111
DB 39 DVVNTKMFELKSR-----LDTL---AQEALLKEQ-QALQTVSLKGT--KVIMKEPPQS 87
QY 112 PLGEMDRARAHVDALRTHLAPYSDELQRLAARLEAKENGARGARLAHYHAKATEHLST 171
DB 88 P-WDRVKDLATVYD-----VLKDSGRDVSQFEGSA----- 118
QY 172 LSEKAKPALEDLROGLLPVLESFKVFSLSALEEYTKKLTQGTCLKLLDNWDSVTSTFSL 231
DB 119 -----LQKLNKLLDNWDSVTSTFSL 141
QY 232 RQLGVPVQEFWDLNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFOKKWQEMELYRQKVE 291
DB 142 RQLGVPVQEFWDLNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFOKKWQEMELYRQKVE 201
QY 292 PLRAELQEGAROKLHELOEKLSPLGEMDRARAHVDALRTHLAPYSDELQRLAARLEA 351
DB 202 PLRAELQEGAROKLHELOEKLSPLGEMDRARAHVDALRTHLAPYSDELQRLAARLEA 261
QY 352 LKENGARGARLAHYHAKATEHLSTSEKAKPALEDLROGLLPVLESFKVFSLSALEEYTKKL 411
DB 262 LKENGARGARLAHYHAKATEHLSTSEKAKPALEDLROGLLPVLESFKVFSLSALEEYTKKL 321
QY 412 NTQ 414
DB 322 NTQ 324

RESULT 6
US-09-987-107-54
; Sequence 54, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pT7H6 Trip-A-Apo A1 K9A K15A - AmpR plasmid
US-09-987-107-54

Query Match 49.6%; Score 1051; DB 9; Length 316;
Best Local Similarity 54.9%; Pred. No. 1.6e-52;
Matches 236; Conservative 22; Mismatches 42; Indels 130; Gaps 9;
QY 1 MGHSHHHH-----IEGRKLLDNWDSVTSTFSLKRLQGLGPTVQTEFWNDL 44
DB 1 MGSHHHHHSGSIOGRSGTEPTQPKAIVNAKADVVNTKMFELKSR-----DTL 52
QY 45 EKETGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLH 104
DB 53 AOEVALLEQQAQVSLKGSDEPP-----QSPW-----81
QY 105 ELQEKLSPLGEEMDRARAHVDALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAK 164
DB 82 -----DRVKDLATVYD-----VLKDSGROYVSQFEGS 109
QY 165 ATEHLSTLSEKAKPALEDLROGLLPVLESFVLSALEEYTKLNTQGTFLKLLDNWDSV 224
DB 110 A-----LGKQLNLKLLDNWDSV 126
QY 225 TSTFSLRQGLGPTVQTEFWNDLEKETEGRLQEMSKDLEEVKAKVQPYLDDFQKKWQEME 284
DB 127 TSTFSLRQGLGPTVQTEFWNDLEKETEGRLQEMSKDLEEVKAKVQPYLDDFQKKWQEME 186
QY 285 LYRQKVEPLRAELQEGARQKLHELOEKLSPLEEMDRARAHVDALRTHLAPYSDELRLQ 344
DB 187 LYRQKVEPLRAELQEGARQKLHELOEKLSPLEEMDRARAHVDALRTHLAPYSDELRLQ 246
QY 345 LAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLROGLLPVLESFVLSAL 404
DB 247 LAARLEALKENGARLAAYHAKATEHLSTLSEKAKPALEDLROGLLPVLESFVLSAL 306
QY 405 EYTKKLLNTQ 414
DB 307 EYTKKLLNTQ 316

RESULT 7
US-09-987-107-66
; Sequence 66, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT FILING DATE: 2001-11-13
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pT7H6 Trip-A-Tn-Apo A1 final K9AK15A - AmpR plasmid
US-09-987-107-66

Query Match 49.6%; Score 1051; DB 9; Length 324;
Best Local Similarity 56.3%; Pred. No. 1.7e-52;
Matches 238; Conservative 30; Mismatches 47; Indels 108; Gaps 11;
QY 1 MGHSHHHH-----IEGRKLLDNWDSVTSTFSLKRLQGLGPTVQTEFWNDLEKETEGRLQ 53
DB 1 MGSHHHHHSGSIOGRSGTE-----PPTQK-----PKAIVNAKA 38
QY 54 EM--SKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELOEKL 111
DB 39 DVVNTKMFELKSR-----LDLTL-----AOEVALLEQ-QALQTVSLKGT--KVHMKPEPPQS 87
QY 112 PLGEEMDRARAHVDALRTHLAPYSDELRLQRLAARLEALKENGARLAAYHAKATEHLST 171
DB 88 P-WDRVKDLATVYD-----VLKDSGRDYVSQFEGSA-----118
QY 172 LSEKAKPALEDLROGLLPVLESFVLSALEEYTKLNTQGTFLKLLDNWDSVTSTFSLK 231
DB 119 -----LGKQLNLKLLDNWDSVTSTFSLK 141
QY 232 RQGLGPTVQTEFWNDLEKETEGRLQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVE 291
DB 142 RQGLGPTVQTEFWNDLEKETEGRLQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVE 201
QY 292 PLRAELQEGARQKLHELOEKLSPLEEMDRARAHVDALRTHLAPYSDELRLQRLAARLEA 351
DB 202 PLRAELQEGARQKLHELOEKLSPLEEMDRARAHVDALRTHLAPYSDELRLQRLAARLEA 261
QY 352 LKENGARLAAYHAKATEHLSTLSEKAKPALEDLROGLLPVLESFVLSALEEYTKKL 411
DB 262 LKENGARLAAYHAKATEHLSTLSEKAKPALEDLROGLLPVLESFVLSALEEYTKKL 321
QY 412 NTQ 414
DB 322 NTQ 324

RESULT 8
US-09-987-107-58
; Sequence 58, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT FILING DATE: 2001-11-13
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pT7H6 Trip-A-Fn-Apo A1-final - AmpR plasmid
US-09-987-107-58

Query Match 49.6%; Score 1049.5; DB 9; Length 323;
Best Local Similarity 56.4%; Pred. No. 2e-52;
Matches 235; Conservative 24; Mismatches 61; Indels 97; Gaps 8;
QY 1 MG-HHHHHHIEGRKLLDNWDSVTSTFSLKRLQGLGPTVQTEFWNDLEKETEGRLQEMSKDL 59
DB 1 MGSHHHHHSGS-----GSIQGRSFGTEPTQPK 31
QY 60 EEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHELOEKLSPLEEMDR 119

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Db 32 KIVNAK-----KSRDLTL---AQEVALLKEQQAQVLSLKGTSQD 81
QY 120 RARAHVDALRTHLAPYS--DELQRRLAARLALKENGARLAAYHAKATEHLSLSEKAK 177
Db 82 E-----PPQSPWDRVKDLATVYVDVKDGRDYVSQFEGSA----- 117
QY 178 PALEDLROGLLPVLESFKVSLSALEEYTKKLTNTOGTLKLDNDWDSVTSTFSKLRQGLGP 237
Db 118 -----LGRQLNKLKLDNDWDSVTSTFSKLRQGLGP 146
QY 238 VTQEFWDNLEKTEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAEL 297
Db 147 VTQEFWDNLEKTEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAEL 206
QY 298 QEGAROKLHELOEKLSPGCEMRDRARAHVDALRTHLAPYSDELQRRLAARLALKENG 357
Db 207 QEGAROKLHELOEKLSPGCEMRDRARAHVDALRTHLAPYSDELQRRLAARLALKENG 266
QY 358 ARLAEYHAKATEHLSLSEKAKPALEDLROGLLPVLESFKVSLSALEEYTKKLTNTQ 414
Db 267 ARLAEYHAKATEHLSLSEKAKPALEDLROGLLPVLESFKVSLSALEEYTKKLTNTQ 323

RESULT 9
US-09-987-107-56
; Sequence 56, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 56
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pT7H6 Trip-A-Fn-Apo A1 - AmpR plasmid
US-09-987-107-56

Query Match 49.5%; Score 1047.5; DB 9; Length 323;
Best Local Similarity 56.4%; Pred. No. 2.6e-52;
Matches 235; Conservative 23; Mismatches 62; Indels 97; Gaps 8;

QY 1 MG-HHHHHHTEGRLKLDNDWDSVTSTFSKLRQGLGPVTQEFWDNLEKTEGLRQEMSKDL 59
Db 1 MGSHHHHHHSGS-----GSIQGRSPGTEPPTQPK 31

QY 60 EEVAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQEGAROKLHELOEKLSPGCEMRD 119
Db 32 KIVNAK-----KSRDLTL---AQEVALLKEQQAQVLSLKGSSGHD 81
QY 120 RARAHVDALRTHLAPYS--DELQRRLAARLALKENGARLAAYHAKATEHLSLSEKAK 177
Db 82 E-----PPQSPWDRVKDLATVYVDVKDGRDYVSQFEGSA----- 117
QY 178 PALEDLROGLLPVLESFKVSLSALEEYTKKLTNTOGTLKLDNDWDSVTSTFSKLRQGLGP 237
Db 118 -----LGRQLNKLKLDNDWDSVTSTFSKLRQGLGP 146
QY 238 VTQEFWDNLEKTEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAEL 297
Db 267 ARLAEYHAKATEHLSLSEKAKPALEDLROGLLPVLESFKVSLSALEEYTKKLTNTQ 323
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Db 147 VTQEFWDNLEKTEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAEL 206
QY 298 QEGAROKLHELOEKLSPGCEMRDRARAHVDALRTHLAPYSDELQRRLAARLALKENG 357
Db 207 QEGAROKLHELOEKLSPGCEMRDRARAHVDALRTHLAPYSDELQRRLAARLALKENG 266
QY 358 ARLAEYHAKATEHLSLSEKAKPALEDLROGLLPVLESFKVSLSALEEYTKKLTNTQ 414
Db 267 ARLAEYHAKATEHLSLSEKAKPALEDLROGLLPVLESFKVSLSALEEYTKKLTNTQ 323

RESULT 10
US-09-987-107-60
; Sequence 60, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 60
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pT7H6 Trip-A-Fn-Apo A1 final K9AK15A - AmpR plasmid
US-09-987-107-60

Query Match 49.4%; Score 1045.5; DB 9; Length 323;
Best Local Similarity 72.9%; Pred. No. 3.4e-52;
Matches 226; Conservative 19; Mismatches 53; Indels 12; Gaps 4;

QY 111 SPLGCEMRDRARAHVDALRTHLAPYSDELQRRLAARLALKENGARLAAYHAKATEHLS 170
Db 20 SPCTEPTQPKAIVNAKADV---NTKMFEEKSLRDLTLAGQ-VALLKEQQAQVLSLK 75
QY 171 TLSEKAKP-----ALEDLRQGLLPVLESFKVSLSALEEYTKKLTNTOGTLKLDNDWDSV 224
Db 76 GTSQDEPPQSPWDRVKDLATVYVDVKDGRDYVSQFE--GSALGKOLNKLKLDNDWDSV 133
QY 225 TSTFSKLRQGLGPVTQEFWDNLEKTEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEME 284
Db 134 TSTFSKLRQGLGPVTQEFWDNLEKTEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEME 193
QY 285 LYRQKVEPLRAELQEGAROKLHELOEKLSPGCEMRDRARAHVDALRTHLAPYSDELQR 344
Db 194 LYRQKVEPLRAELQEGAROKLHELOEKLSPGCEMRDRARAHVDALRTHLAPYSDELQR 253
QY 345 LAARLALKENGARLAAYHAKATEHLSLSEKAKPALEDLROGLLPVLESFKVSLSALE 404
Db 254 LAARLALKENGARLAAYHAKATEHLSLSEKAKPALEDLROGLLPVLESFKVSLSALE 313
QY 405 EYTKKLTNTQ 414
Db 314 EYTKKLTNTQ 323

RESULT 11
US-09-987-107-8
; Sequence 8, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
```

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; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(56)
; OTHER INFORMATION: Trimerisation module from tetranectin
; NAME/KEY: misc_feature
; LOCATION: (57)..(61)
; OTHER INFORMATION: Fibronection based linker
; NAME/KEY: misc_feature
; LOCATION: (62)..(304)
; OTHER INFORMATION: Mature Apo A1
; US-09-987-107-8
;
Query Match 49.28; Score 1042; DB 9; Length 304;
Best Local Similarity 72.98; Pred. No. 5e-52;
Matches 226; Conservative 19; Mismatches 53; Indels 12; Gaps 4;

QY 111 SPLGEMDRARAHVDALRTHLAPYSDELQRLAARLEALKENGARLAAYHAKATEHLS 170
Db 1 SPGTEPTQPKAIVNADVV---NTKMEELKSRLDTLAE-VALLKEQQAQTIVSLK 56
QY 171 TLSEKAKP-----ALEDLRQGLLPVLESFKVSLSALEEYTKKLTQGTILKLDNDVSV 224
Db 57 GTSQDEPPQSPWDRVKDLATVYVDVKDGRDYVSQFE--GSALGKQLNKLKLDNDVSV 114
QY 225 TSTFSKLEQLGPTVQTEFWNDLEKETEGLRQEMSKDLEEVKAKVQPYLDDDFQKKWQEME 284
Db 115 TSTFSKLEQLGPTVQTEFWNDLEKETEGLRQEMSKDLEEVKAKVQPYLDDDFQKKWQEME 174
QY 285 LYRQKVEPLRAELQEGARQKLHELQEKLSPLGEMDRARAHVDALRTHLAPYSDELQRL 344
Db 175 LYRQKVEPLRAELQEGARQKLHELQEKLSPLGEMDRARAHVDALRTHLAPYSDELQRL 234
QY 345 LAARLEALKENGARLAAYHAKATEHLSLSEKAKPALEDLROGLLPVLESFKVSLFSLAL 404
Db 235 LAARLEALKENGARLAAYHAKATEHLSLSEKAKPALEDLROGLLPVLESFKVSLFSLAL 294
QY 405 EYTKKLTNQ 414
Db 295 EYTKKLTNQ 304

RESULT 12
US-09-987-107-7
; Sequence 7, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 261
;

; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(56)
; OTHER INFORMATION: Trimerisation module from tetranectin
; NAME/KEY: misc_feature
; LOCATION: (57)..(61)
; OTHER INFORMATION: Fibronection based linker
; NAME/KEY: misc_feature
; LOCATION: (62)..(304)
; OTHER INFORMATION: Mature Apo A1
; US-09-987-107-7
;
Query Match 49.28; Score 1041; DB 9; Length 304;
Best Local Similarity 72.58; Pred. No. 5.7e-52;
Matches 224; Conservative 18; Mismatches 51; Indels 16; Gaps 4;

QY 112 PLGEMDRARAHVDALRTHLAPYSDELQRLAARLEALKENGARLAAYHAKATEHLS 171
Db 6 PPTQPKPKAIVNADVVNT-----KMEELKSRLDTLAE-VALLKEQQAQTIVSLK 57
QY 172 LSEKAKP-----ALEDLRQGLLPVLESFKVSLSALEEYTKKLTQGTILKLDNDVSV 225
Db 58 TSGQDEPPQSPWDRVKDLATVYVDVKDGRDYVSQFE--GSALGKQLNKLKLDNDVSV 115
QY 226 STFSKLEQLGPTVQTEFWNDLEKETEGLRQEMSKDLEEVKAKVQPYLDDDFQKKWQEME 285
Db 116 STFSKLEQLGPTVQTEFWNDLEKETEGLRQEMSKDLEEVKAKVQPYLDDDFQKKWQEME 175
QY 286 YRQKVEPLRAELQEGARQKLHELQEKLSPLGEMDRARAHVDALRTHLAPYSDELQRL 345
Db 176 YRQKVEPLRAELQEGARQKLHELQEKLSPLGEMDRARAHVDALRTHLAPYSDELQRL 235
QY 346 AARLEALKENGARLAAYHAKATEHLSLSEKAKPALEDLROGLLPVLESFKVSLFSLAL 405
Db 236 AARLEALKENGARLAAYHAKATEHLSLSEKAKPALEDLROGLLPVLESFKVSLFSLAL 295
QY 406 EYTKKLTNQ 414
Db 296 EYTKKLTNQ 304

RESULT 13
US-09-987-107-52
; Sequence 52, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 52
; LENGTH: 261
;

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/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: pT7 H6 Fx Cys-Apo A1 plasmid
US-09-987-107-52

Query Match      49.1%; Score 1039.5; DB 9; Length 261;
Best Local Similarity 80.8%; Pred. No. 5.9e-52;
Matches 211; Conservative 0; Mismatches 1; Indels 49; Gaps 2;

QY 1 MGHHHHH---TEGR----- 12
Db 1 MSHHHHHHSGTEGRCDDPQSPWDRVKDLATYVVDVKDSGRDYVSQFEGSALGKQL 60

QY 13 -LKLLDNWDSVSTFSKLRQGLPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLD 71
Db 61 NLKLLDNWDSVSTFSKLRQGLPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLD 120

QY 72 DFQKKQWQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGGEEMDRARAHVDALRTH 131
Db 121 DFQKKQWQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLGGEEMDRARAHVDALRTH 180

QY 132 LAPYSDLRORLAARLEALKENGARLAIEYHAKATEHLSLSEKAKPALEDLRQGLLPVL 191
Db 181 LAPYSDLRORLAARLEALKENGARLAIEYHAKATEHLSLSEKAKPALEDLRQGLLPVL 240

QY 192 ESFKVSFSLSALEYTKKLTQ 212
Db 241 ESFKVSFSLSALEYTKKLTQ 261

RESULT 14
US-09-987-107-6
; Sequence 6, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(58)
; OTHER INFORMATION: Trimerisation module from tetranectin
; NAME/KEY: misc_feature
; LOCATION: (59)..(61)
; OTHER INFORMATION: Linker
; NAME/KEY: misc_feature
; LOCATION: (62)..(304)
; OTHER INFORMATION: Mature Apo A1
US-09-987-107-6

Query Match      49.0%; Score 1038; DB 9; Length 304;
Best Local Similarity 72.5%; Pred. No. 8.3e-52;
Matches 224; Conservative 17; Mismatches 52; Indels 16; Gaps 4;

QY 112 PLGGEEMDRARAHVDALRTHLAPYSDELQRLAARLEALKENGARLAIEYHAKATEHLS 171
Db 6 PPTQPKRIVNAKKDVNT-----KMFELKSRDLTQAE-VALLKEQALQTVSLKG 57

/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: pT7 H6 Fx Cys-Apo A1 plasmid
US-09-987-107-52

Query Match      48.9%; Score 1036.5; DB 9; Length 301;
Best Local Similarity 73.3%; Pred. No. 1e-51;
Matches 225; Conservative 18; Mismatches 55; Indels 9; Gaps 4;

QY 111 SPLGGEEMDRARAHVDALRTHLAPYSDELQRLAARLEALKENGARLAIEYHAKATEHLS 170
Db 1 SPCTEPTQPKRAIVNAKADV--NTKMFELKSRDLTQAE-VALLKEQALQTVSLK 56

QY 171 TLSEKAK---PALEDLRQGLLPVLESFKVSFSLSALEYTKKLTQGLKLLDNWDSVTST 227
Db 57 GSDEPPQSPWDRVKDLATYVVDVKDSGRDYVSQFE--GSALGKQLNLKLLDNWDSVTST 114

QY 228 FSKLRQGLPVTQEFWDNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFQKKQWQEMEL 287
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Db	115	FSKLREQLPVTQEFWDNLEKETEGLEQEMSKDLEEVKAKVQPYLDDFOKKWQEMELYR	174
Qy	288	QKVEPLRAELQEGARQKLHELQEKLSPLGEMRDRARAHVDALRTHLAPYSDELQRLAA	347
Db	175	QKVEPLRAELQEGARQKLHELQEKLSPLGEMRDRARAHVDALRTHLAPYSDELQRLAA	234
Qy	348	RLEALKENGARLAELYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFSLALEY	407
Db	235	RLEALKENGARLAELYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFSLALEY	294
Qy	408	TKKLNTQ	414
Db	295	TKKLNTQ	301

Search completed: April 30, 2003, 15:19:27
Job time : 48 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 30, 2003, 15:10:37 ; Search time 22 Seconds
(without alignments)
1809.075 Million cell updates/sec

Title: US-09-990-087-17
Perfect score: 2118
Sequence: 1 MGHHHHHIEGRLLKLLDND.....SFKVSFLSALEETKKLNTQ 414

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1024	48.3	267	1 LPHUA1	apolipoprotein A-I
2	991.5	46.8	267	1 A26529	apolipoprotein A-I
3	991.5	46.8	267	2 JS0079	apolipoprotein A-I
4	860.5	40.6	266	1 LPDGA1	apolipoprotein A-I
5	837	39.5	266	1 LPRB1Z	apolipoprotein A-I
6	825.5	39.0	241	2 A24998	apolipoprotein A-I
7	818.5	38.6	265	1 LPRB1B	apolipoprotein A-I
8	809	38.2	265	2 A46018	apolipoprotein A-I
9	809	38.2	265	2 JT0672	apolipoprotein A-I
10	803	37.9	265	2 A56858	apolipoprotein A-I
11	796.5	37.6	264	2 S31394	apolipoprotein A-I
12	789.5	37.3	231	2 JQ0704	apolipoprotein A-I
13	653	30.8	284	2 S22420	apolipoprotein A-I
14	647	30.5	262	2 JCI237	apolipoprotein A-I
15	617.5	29.2	164	2 S21830	apolipoprotein A-I
16	591	27.9	259	2 A24700	apolipoprotein A-I
17	505.5	23.9	246	2 A61448	apolipoprotein A-I
18	491.5	23.2	264	1 LPCHA1	apolipoprotein A-I
19	470.5	22.2	264	2 JC3456	apolipoprotein A-I
20	350.5	16.5	429	2 S29565	apolipoprotein A-I
21	339.5	16.0	401	2 A47141	apolipoprotein A-I
22	324.5	15.3	396	1 LPHUA4	apolipoprotein A-I
23	291.5	13.8	391	1 LPRTA4	apolipoprotein A-I
24	283	13.4	399	2 C40892	apolipoprotein A-I
25	279	13.2	391	2 B40892	apolipoprotein A-I
26	279	13.2	395	2 A40892	apolipoprotein A-I
27	275	13.0	394	2 A25281	apolipoprotein A-I
28	251	11.9	1547	2 T28657	blackjack protein,
29	222	10.5	1938	2 JC5421	smooth muscle myosin

30	222	10.5	1972	2 JC5420	smooth muscle myosin
31	219.5	10.4	1410	1 A57013	early endosome ant
32	216.5	10.2	1039	2 S18199	myosin heavy chain
33	214	10.1	3187	2 JC5837	364K Golgi complex
34	209.5	9.9	1979	1 S03166	myosin heavy chain
35	209	9.9	1999	1 S21801	myosin heavy chain
36	208.5	9.8	1934	2 I48153	myosin heavy chain
37	208	9.8	880	2 F75103	conserved hypotet
38	208	9.8	886	2 H69378	conserved hypotet
39	208	9.8	978	2 A70387	conserved hypotet
40	207.5	9.8	1938	2 A59293	skeletal myosin he
41	207	9.8	1972	1 A41604	myosin heavy chain
42	205.5	9.7	1935	2 A5286	myosin heavy chain
43	205.5	9.7	2007	1 B43402	myosin heavy chain
44	205	9.7	1935	1 A37102	myosin beta heavy
45	204.5	9.7	1938	1 A40997	myosin heavy chain

ALIGNMENTS

RESULT 1

LPHUA1

apolipoprotein A-I precursor [validated] - human

N:Alternate names: apoA-I-2; apoA-I-4; preproapoA-I; prostacyclin stabilizing factor

C:Species: Homo sapiens (man)

C>Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 08-Dec-2000

C:Accession: A90947; B90947; S02373; A93465; A21147; A93519; B93519; A93472; A94010; 6197

R:Seilhamer, J.J.; Protter, A.A.; Frossard, P.; Levy-Wilson, B.

DNA 3, 309-317, 1984

A:Title: Isolation and DNA sequence of full-length cDNA and of the entire gene for hu

A:Reference number: A90947; MUID:85026665; PMID:6207999

A:Accession: A90947

A:Molecule type: DNA

A:Residues: 1-267 <SEI>

A:Cross-references: GB:X01038; NID:g28769; PIDN:CAA25519.1; PID:g296635

A:Accession: B90947

A:Molecule type: mRNA

A:Residues: 1-267 <SE2>

A:Cross-references: GB:X01038; NID:g28769; PIDN:CAA25519.1; PID:g296635

R:Makrides, S.C.; Ruiz-Opazo, N.; Hayden, M.; Nussbaum, A.L.; Breslow, J.L.; Zannis,

Eur. J. Biochem. 173, 465-471, 1988

A:Title: Sequence and expression of Tangier apoA-I gene.

A:Reference number: S02373; MUID:86196137; PMID:3129297

A:Accession: S02373

A:Molecule type: DNA

A:Residues: 1-267 <MAK>

A:Cross-references: EMBL:X07496; NID:g28774; PIDN:CAA30377.1; PID:g296729

R:Shoulders, C.C.; Kornblitt, A.R.; Munro, B.S.; Baralle, F.E.

Nucleic Acids Res. 11, 2827-2837, 1983

A:Title: Gene structure of human apolipoprotein A-I.

A:Reference number: A93465; MUID:83220822; PMID:6406984

A:Accession: A93465

A:Molecule type: DNA

A:Residues: 1-267 <SHO>

A:Cross-references: GB:J00098; GB:J00099; GB:J00100; GB:J00101; GB:J03222; GB:K01518;

R:Karathanasis, S.K.; Zannis, V.I.; Breslow, J.L.

Proc. Natl. Acad. Sci. U.S.A. 80, 6147-6151, 1983

A:Title: Isolation and characterization of the human apolipoprotein A-I gene.

A:Reference number: A21147; MUID:84016011; PMID:6413973

A:Accession: A21147

A:Molecule type: DNA

A:Residues: 1-267 <KAR>

A:Cross-references: GB:J00098; GB:J03222; NID:g178765; PIDN:AAB59514.1; PID:g178768

R:Sharpe, C.R.; Stodoli, A.; Shelley, C.S.; Lucero, M.A.; Shoulders, C.C.; Baralle, F.

Nucleic Acids Res. 12, 3917-3932, 1984

A:Title: Human apolipoproteins AI, AII, CII and CIII. cDNA sequences and mRNA abundan

A:Reference number: A93519; MUID:84221405; PMID:6328445

A:Accession: A93519

A:Molecule type: mRNA

A:Residues: 1-267 <SHO>

A:Cross-references: GB:X00566; NID:g28765; PIDN:CAA25232.1; PID:g732753

A:Accession: B93519
 A:Molecule type: DNA
 A:Residues: 1-24 <SH2>
 R:Cheung, P.; Chan, L.
 Nucleic Acids Res. 11, 3703-3715, 1983
 A:Title: Nucleotide sequence of cloned cDNA of human apolipoprotein A-I.
 A:Reference number: A93472; MUID:83220772; PMID:6304641
 A:Accession: A93472
 A:Molecule type: mRNA
 A:Residues: 1-267 <CHE>
 A:Cross-references: GB:J000098; GB:J000099; GB:J00100; GB:J00101; GB:J03222; GB:K01518; GB:R:Law, S.W.; Brewer Jr., H.B.
 Proc. Natl. Acad. Sci. U.S.A. 81, 66-70, 1984
 A:Title: Nucleotide sequence and the encoded amino acids of human apolipoprotein A-I mRNA
 A:Reference number: A94010; MUID:84119464; PMID:6198645
 A:Accession: A94010
 A:Molecule type: mRNA
 A:Residues: 1-267 <LAW>
 A:Cross-references: GB:J00098; GB:J00099; GB:J00100; GB:J00101; GB:J03222; GB:K01518; GB:R:Zannis, V.I.; Karathanasis, S.K.; Keutmann, H.T.; Goldberger, G.; Breslow, J.L.
 Proc. Natl. Acad. Sci. U.S.A. 80, 2574-2578, 1983
 A:Title: Intracellular and extracellular processing of human apolipoprotein A-I: secreted
 A:Reference number: A21118; MUID:83195100; PMID:6405383
 A:Accession: A21118
 A:Molecule type: mRNA
 A:Residues: 1-24 <ZAN>
 R:Brewer Jr., H.B.; Fairwell, T.; Kay, L.; Meng, M.; Ronan, R.; Law, S.; Light, J.A.
 Biochem. Biophys. Res. Commun. 113, 526-532, 1983
 A:Title: Human plasma preapoA-I: isolation and amino-terminal sequence.
 A:Reference number: A90112; MUID:83256553; PMID:6409108
 A:Accession: A90112
 A:Molecule type: protein
 A:Residues: 19-27 <BRE>
 R:Brewer Jr., H.B.; Fairwell, T.; LaRue, A.; Ronan, R.; Houser, A.; Bronzert, T.J.
 Biochem. Biophys. Res. Commun. 80, 623-630, 1978
 A:Title: The amino acid sequence of human APOA-I, an apolipoprotein isolated from high density lipoproteins.
 A:Reference number: A90209; MUID:78123731; PMID:204308
 A:Accession: A90209
 A:Molecule type: protein
 A:Residues: 25-57, 'O', 59-169, 'OO', 172-267 <BR2>
 R:Yui, Y.; Aoyama, T.; Morishita, H.; Takahashi, M.; Takatsu, Y.; Kawai, C.
 J. Clin. Invest. 82, 803-807, 1988
 A:Title: Serum prostacyclin stabilizing factor is identical to apolipoprotein A-I (Apo A I).
 A:Reference number: A30516; MUID:88331387; PMID:3047170
 A:Accession: A30516
 A:Molecule type: protein
 A:Residues: 25-56 <YUI>
 R:Nichols, W.C.; Dullet, F.E.; Liepnieks, J.; Benson, M.D.
 Biochem. Biophys. Res. Commun. 156, 762-768, 1988
 A:Title: Variant apolipoprotein AI as a major constituent of a human hereditary amyloid.
 A:Reference number: A31582; MUID:89050104; PMID:3142462
 A:Accession: A31582
 A:Molecule type: protein
 A:Residues: 25-49, 'R', 51-85, 'D', 87-107 <NIC>
 A:Note: variant sequence from patient with familial amyloidotic polyneuropathy type III
 R:Manjunath, P.; Marcel, Y.L.; Uma, J.; Seidah, N.G.; Chretien, M.; Chapdelaine, A.
 J. Biol. Chem. 264, 16853-16857, 1989
 A:Title: Apolipoprotein A-I binds to a family of bovine seminal plasma proteins.
 A:Reference number: A34409; MUID:89380318; PMID:2506184
 A:Accession: A34409
 A:Molecule type: protein
 A:Residues: 25-48 <MAN>
 R:Stoffel, W.; Binczek, E.
 Biol. Chem. Hoppe-Seyler 369, 1055-1063, 1988
 A:Title: Structural requirements of human preapoApolipoprotein AI for translocation and
 A:Reference number: S02737; MUID:89149597; PMID:3228490
 A:Accession: S02737
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-6, 'AV', 9, 'LV', 12-29 <STO>
 A:Note: part of this sequence, including the amino end of the mature protein, was confirmed
 R:Stoffel, W.; Binczek, E.
 Biol. Chem. Hoppe-Seyler 372, 481-488, 1991
 A:Title: Transient expression of wild type and mutant human apolipoprotein AI in COS
 A:Reference number: S16197; MUID:92029676; PMID:1930731
 A:Contents: annotation; extension of studies in reference S02737
 R:Stoffel, W.; Kruger, E.; Deutzmann, R.
 Hoppe-Seyler's Z. Physiol. Chem. 364, 227-237, 1983
 A:Title: Cell-free translation of human liver apolipoprotein AI and AII mRNA processes
 A:Reference number: A19913; MUID:83236195; PMID:6407957
 A:Accession: B19913
 A:Molecule type: protein
 A:Residues: 1-6, 'X', 8-13, 'XXX', 17-18, 'XX', 21, 'X', 23-25, 'X', 27-29 <SW2>
 R:Ehnholm, C.; Bozas, S.E.; Tenkanen, H.; Kirsbaum, L.; Metsä, J.; Murphy, B.; Walke
 Biochim. Biophys. Acta 1086, 255-260, 1991
 A:Title: The apolipoprotein A-I binding protein of placenta and the SP-40.40 protein
 A:Reference number: A56815; MUID:92075698; PMID:1742316
 A:Accession: A56815
 A:Molecule type: protein
 A:Residues: 25-31, 'P', 33 <EHN>
 A:Experimental source: serum
 A:Note: sequence extracted from NCBI backbone (NCBIP:69759)
 A:Note: 32-Trip was also found
 R:Kunitake, S.T.; Carilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vigne, J.; Kane, J.P.
 Biochemistry 33, 1988-1993, 1994
 A:Title: Identification of proteins associated with apolipoprotein A-I-containing lip
 A:Reference number: A54223; MUID:94162201; PMID:8117655
 A:Accession: A54223
 A:Molecule type: protein
 A:Residues: 25-39 <KUN>
 R:Mogul'sky, N.; Roobol, C.; Loriau, R.; Guillaume, J.P.; Jacobs, P.; Cravador, A.;
 DNA 8, 429-436, 1989
 A:Title: Production of human recombinant proapolipoprotein A-I in *Escherichia coli*: p
 A:Reference number: I39476; MUID:89377481; PMID:2673706
 A:Accession: I39476
 A:Molecule type: mRNA
 A:Residues: 19-267 <RES>
 A:Cross-references: GB:M25066; NID:gl78774; PIDN:AAA51747.1; PID:gl78775
 R:Higuchi, K.; Law, S.W.; Hoeg, J.M.; Schumacher, U.K.; Meglin, N.; Brewer, H.B.
 J. Biol. Chem. 263, 18530-18536, 1988
 A:Title: Tissue-specific expression of apolipoprotein A-I (ApoA-I) is regulated by th
 A:Reference number: I39475; MUID:89054040; PMID:3142880
 A:Accession: I39475
 A:Molecule type: DNA
 A:Residues: 1-14 <RE2>
 A:Cross-references: GB:J04066; NID:gl78763; PIDN:AAA51746.1; PID:g553183
 R:Breslow, J.L.
 Annu. Rev. Biochem. 54, 699-727, 1985
 A:Title: Human apolipoprotein molecular biology and genetic variation.
 A:Reference number: A90042; MUID:85278004; PMID:3896129
 A:Contents: annotation; review of sequences, variants and gene location
 R:Hoeg, J.M.; Meng, M.S.; Ronan, R.; Fairwell, T.; Brewer Jr., H.B.
 J. Biol. Chem. 261, 3911-3914, 1986
 A:Title: Human apolipoprotein A-I. Post-translational modification by fatty acid acyl
 A:Reference number: A92577; MUID:86140194; PMID:3005308
 A:Contents: annotation; acylation with palmitate
 A:Note: an undetermined serine or threonine is acylated by fatty acid; the acylating
 R:Law, S.W.; Brewer, H.B.
 J. Biol. Chem. 260, 12810-12814, 1985
 A:Title: Tangier disease: The complete mRNA sequence encoding for preapoA-A-I.
 A:Reference number: I55236; MUID:86008382; PMID:2995392
 A:Accession: I55236
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-143, 'D', 145-267 <RE3>
 A:Cross-references: GB:M11791; NID:gl78776; PIDN:AAA35545.1; PID:gl78777
 C:Comment: Apolipoprotein A-I precursor is synthesized in the liver and small intestine
 C:Genetics: HDL in plasma.
 A:Gene: GDB:APOA1
 A:Cross-references: GDB:1119684; OMIM:107680
 A:Map position: 11q23.3-11q23.3
 A:Introns: 15/1; 67/2
 C:Function:
 A:Description: participates in the reverse transport of cholesterol from tissues to t
 sterol acyltransferase (LCAT); noncovalently binds and stabilizes prostacyclin (PGI-2

Note: sequence extracted from NCBI backbone (NCBIN:129509, NCBIIP:129511)

32 DRVKEFATVYVDAIKDS

QY 197 SFLSALEEYTKKLTQGTGLKLLDNWDSVTSTFSKLRQGLGPVTOEFWDNLEKETEGLRQE 256
Db 59 ---SALGKHUK-----LKLNDWDSLGSTFTKVRQGLGPVTOEFWDNLEKETEGLRQE 108
QY 257 MSKDLSEEVKAKVQPYLDLDFQKKQWQEMELYRQKVEPLRAELQEGARQKHLQELKLSPLG 316
Db 109 MSKDLSEEVKAKVQPYLDLDFQKKQWQEMELYRQKVEPLRAELQEGARQKHLQELKLSPLA 168
QY 317 EEMDRARAHVDALRTHLAPYSDELRLQRLAARLEALKENGGAARLAHYHAKATEHLSTLSE 376
Db 169 EELRDLRAHVAALRQHVAPYSDDLQRLAARLEALKENGGAARLAHYHAKATEHLSTLSE 227
QY 377 KAKPALEDLROGLLPVLESFVSKVFLSALEEYTKKLTNQ 414
Db 228 KAKPALEDLROGLLPVLESFVSKVFLSALEEYTKKLTNQ 265
RESULT 10
A56858
apolipoprotein A-I precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 05-Jan-1996 #sequence_revision 23-Aug-1997 #text_change 13-Aug-1999
C:Accession: I45853; A56858; A34649
R:O'Huigin, C.; Chan, L.; Li, W.
Mol. Biol. Evol. 7, 327-339, 1990
A:Title: Cloning and sequencing of bovine apolipoprotein A-I cDNA and molecular evolution
A:Reference number: I45853; MUID:90348478; PMID:2117227
A:Accession: I45853
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-265 <ORF>
A:Cross-references: GB:M35870; NID:g162677; PIDN:AAA30381.1; PID:g162678
R:Sparrow, D.A.; Lee, B.R.; Laplaud, P.M.; Aubeiron, S.; Bauchart, D.; Chapman, M.J.; G
Biochim. Biophys. Acta 1223, 145-150, 1992
A:Title: Plasma lipid transport in the prerinant calf, Bos spp: primary structure of h
A:Reference number: A56858; MUID:92153895; PMID:1739745
A:Accession: A56858
A:Status: preliminary
A:Molecule type: protein
A:Residues: 19-184, 'OL', 187-265 <SPA>
A:Experimental source: Friesian-Holstein male calves aged 2-4 weeks
A:Note: sequence extracted from NCBI backbone (NCBIP:83520)
R:Aubeiron, S.; Sparrow, D.A.; Beaubatie, L.; Bauchart, D.; Sparrow, J.T.; Laplaud, P.M.
Biochem. Biophys. Res. Commun. 166, 833-839, 1990
A:Title: Characterization and amino-terminal sequence of apolipoprotein AI from plasma h
A:Reference number: A34649; MUID:90147795; PMID:2105728
A:Accession: A34649
A:Molecule type: protein
A:Residues: 25-70 <AUB>
A:Experimental source: Friesian-Holstein male calves aged 2-4 weeks
A:Superfamily: apolipoprotein A-I
A:Keywords: lipid binding; lipoprotein
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-265/Product: apolipoprotein A-I #status experimental <MAT>
Query Match 37.9%; Score 803; DB 2; Length 265;
Best Local Similarity 58.6%; Pred. No. 8.6e-31;
Matches 163; Conservative 29; Mismatches 42; Indels 44; Gaps 2;
QY 137 DELRQRLAARLEALKENGGAARLAHYHAKATEHLSTLSEKAKPALEDLROGLLPVLESFV 196
Db 32 DRVKDFATVYVDAIKDSGRDYVAQFEASALGHLN----- 60
QY 197 SFLSALEEYTKKLTQGTGLKLLDNWDSVTSTFSKLRQGLGPVTOEFWDNLEKETEGLRQE 256
Db 61 -----LGKQLNLKLLDNWDTLASTLSKVRQGLGPVTOEFWDNLEKETASLRQE 108
QY 257 MSKDLSEEVKAKVQPYLDLDFQKKQWQEMELYRQKVEPLRAELQEGARQKHLQELKLSPLG 316
Db 109 MHKDLSEEVKAKVQPYLDLDFQKKQWQEMELYRQKVEPLRAELQEGARQKHLQELKLSPLA 168
QY 317 EEMDRARAHVDALRTHLAPYSDELRLQRLAARLEALKENGGAARLAHYHAKATEHLSTLSE 376

Db 169 QELDRARAHVETLRQHVAPYSDDLQRLAARLEALKENGGAARLAHYHAKASEQLKALGE 227
QY 377 KAKPALEDLROGLLPVLESFVSKVFLSALEEYTKKLTNQ 414
Db 228 KAKPALEDLROGLLPVLESFVSKVFLSALEEYTKKLTNQ 265
RESULT 11
S31394
apolipoprotein A-I - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
C:Accession: S31394
R:Moehel, B.; Flach, R.; Weiss, B.; Weiler-Guettler, H.; Frey, A.; Zinke, H.; Gassen
submitted to the EMBL Data Library, November 1992
A:Description: Genomic organization of the porcine apolipoprotein A1 gene and study o
A:Reference number: S31394
A:Accession: S31394
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-264 <MOE>
A:Cross-references: EMBL:X69477; NID:g1889; PIDN:CAA49234.1; PID:g1890
C:Superfamily: apolipoprotein A-I
Query Match 37.6%; Score 796.5; DB 2; Length 264;
Best Local Similarity 59.9%; Pred. No. 1.7e-30;
Matches 167; Conservative 27; Mismatches 38; Indels 47; Gaps 4;
QY 137 DELRQRLAARLEALKENGGAARLAHYHAKAT-EHLSTLSEKAKPALEDLROGLLPVLESFV 195
Db 32 DRVKDFATVYVDAIKDSGRDYVAQFEASALGHLN----- 66
QY 196 VPSLSALEEYTKKLTQGTGLKLLDNWDSVTSTFSKLRQGLGPVTOEFWDNLEKETEGLRQ 255
Db 67 -----LKLNDWDSLGSTFTKVRQGLGPVTOEFWDNLEKETALRQ 107
QY 256 ENSKDLSEEVKAKVQPYLDLDFQKKQWQEMELYRQKVEPLRAELQEGARQKHLQELKLSPL 315
Db 108 ENSKDLSEEVKAKVQPYLDLDFQKKQWQEMELYRQKVEPLRAELQEGARQKHLQELKLSPL 166
QY 316 GEMDRARAHVDALRTHLAPYSDELRLQRLAARLEALKENGGAARLAHYHAKATEHLSTLSE 375
Db 167 AEELRDLRAHVAALRQHVAPYSDDLQRLAARLEALKENGGAARLAHYHAKATEHLSTLSE 225
QY 376 EKAKPALEDLROGLLPVLESFVSKVFLSALEEYTKKLTNQ 414
Db 226 EKAKPALEDLROGLLPVLENLKVSIILAAIDEASKKLNAQ 264
RESULT 12
JQ0704
apolipoprotein A-I - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 28-Oct-1994
C:Accession: JQ0704
R:Weiler-Guettler, H.; Sommerfeldt, M.; Papandrikopoulou, A.; Mischek, U.; Bonitz, D.
J. Neurochem. 54, 444-450, 1990
A:Title: Synthesis of apolipoprotein A-I in pig brain microvascular endothelial cells
A:Reference number: JQ0704; MUID:90132667; PMID:2105375
A:Accession: JQ0704
A:Molecule type: mRNA
A:Residues: 1-231 <WEI>
A:Note: the authors translated the codon CAG for residue 124 as His and GAC for resid
C:Superfamily: apolipoprotein A-I
C:Keywords: cholesterol metabolism; HDL; lipid binding; lipid transport; lipoprotein;
Query Match 37.3%; Score 789.5; DB 2; Length 231;
Best Local Similarity 61.3%; Pred. No. 3.1e-30;
Matches 165; Conservative 26; Mismatches 31; Indels 47; Gaps 4;
QY 147 LEALKENGGAARLAHYHAKAT-EHLSTLSEKAKPALEDLROGLLPVLESFVSKVFLSALEEY 205

Db	9	VDAIKDSGRDYVAQFASALGKHNLN-----	33
QY	206	TKKLNTQGTTLKLNDNWDSTVTSFKLRQLQGLPVTQEFWDNLKETEGLRQEMSKDLEEVK	265
Db	34	-----LKLNDNWSLGSFTFKVREQLQGLPVTQEFWDNLKETEALRQKMSKDLEEVK	84
QY	266	AKVQPYLDDFOKKWQEMELRYQKVYPLRAELQEGARQKLHELOBKLSPLQEGMRDRARA	325
Db	85	KKVQPYLDDFOFNKWQEMETYPQKM-PLGAEPREGARQVQLOBKLSPLAEEKRLURA	143
QY	326	HVDALRTHLPASYDELRQLRAARLEALKENGARLAEYHAKATEHLSLTSEKAKPALEDL	385
Db	144	HVAALRQHVPYSDLLRQRWAARFEALKE-GGDSLAEYQAKAQEQKALGEKAKPALEDL	202
QY	386	RQGLLPVLESFKVSVFLSALAEYTKKLNTQ	414
Db	203	RQGLLPVLENLKVSILAAIDEASKILNAQ	231

RESULT 13

S22420

apolipoprotein A-I precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999

C:Accession: S22420; S22421; A44364

R:Stofel, W.; Mueller, R.; Binczek, E.; Hofmann, K.

Biol. Chem. Hoppe-Seyler 373, 187-193, 1992

A:Title: Mouse apolipoprotein AI. cDNA-derived primary structure, gene organisation and

A:Reference number: S22420; MUID:92281682; PMID:1596360

A:Accession: S22420

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-264 <STO>

A:Cross-references: EMBL:X64262; NID:g50014; PIDN:CAA45560.1; PID:g50015

A:Accession: S22421

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-264 <ST2>

A:Cross-references: EMBL:X64263; NID:g50020; PIDN:CAA45561.1; PID:g50021

R:Januzzi, J.L.; Azrolan, N.; O'Connell, A.; Aalto-Setälä, K.; Breslow, J.L.

Genomics 14, 1081-1088, 1992

A:Title: Characterization of the mouse apolipoprotein Apoa-1/Apoc-3 gene locus: genomic

A:Reference number: A44364; MUID:93122774; PMID:1478650

A:Accession: A44364

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-264 <JAN>

A>Note: sequence extracted from NCBI backbone (NCBIN:122400, NCBIPI:122407)

C:Genetics:

A:introns: 15/1; 66/2

C:superfamily: apolipoprotein A-I

	Query Match	30.8%	Score 653;	DB 2;	Length 264;
	Best Local Similarity	59.0%;	Pred. No. 7.3e-24;		
	Matches 128;	Conservative 37;	Mismatches 48;	Indels 4;	Gaps 2;
QY	198	FLSALAEYYTKKLTNQGTGLKLIDNDWSVTSFNSKLREQLGPGVTQEFWDNLXKETEGLRDEM	257		
Ddb	52	YVSQFE---SSSLGGQGLNLLNLENNWDTLGSIVSQLGRLPLTRDFWNLERKETDWRDEM	109		
QY	258	SKDLBEVKAKVPQYLDLFQFKWOEEMELYRQKYVEPLRAELGEARQKHLHEQKLSPLGCE	317		
Ddb	110	NKDLEEVRQKVQPYLDLFQFKWKVEDVELYRQKVAPLGAELQESARQKQLQGLQRULSPVAE	169		
QY	318	EMROARAHVDAKTHLAPYSDELRRORLAARLEALKENGAGRIAEVHKATETHSTLSEK	377		
Ddb	170	EFRDMRTHVDLSRTLQAPHSEQMRSQAORTAELASN--PTLNETHYHTRAKTHLTATLKEK	227		
QY	378	AKPALEDLRQGLLPVLSEFVKVFSLSALAEYYTKKLTNQ	414		
Ddb	228	ARPAAEDLRHSILPMLETTLTKAQSVIIDKASETTTAAQ	264		

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RESULT 14 -
apolipoprotein A-I precursor - mouse
JC1237
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-1993
C:Accession: JC1237
E:Boyle, I.P.; Marotti, K.R.
Gene 117, 243-247, 1992
A:Title: Structure of the murine gene encoding apolipoprotein A-I.
A:Reference number: JC1237; PMID:92347700; PMID:1639271
A:Accession: JC1237
A:Molecule type: DNA
A:Residues: 1-262 <BOY>
A:Cross-references: GB:M77801
C:Genetics:
C:Gene: ApoA-I
A:Introns: 15/1; 66/2
C:Superfamily: apolipoprotein A-I
C:Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid tr
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-262/Product: apolipoprotein A-I #status predicted <MAT>

```

	Query Match	30.5%;	Score 647;	DB 2;	Length 262;
	Best Local Similarity	61.1%;	Pred. No. 1.4e-23;		
	Matches 127;	Conservative 33;	Mismatches 44;	Indels 4;	Gaps
QY	198	FISALEEYTKLNTQGTLLDNWDVSVTSTFSKLRQLGPGPYTOFNDWLNKEETGLRQEM	257	:	:
Db	52	YVSQFE--SSSLGOQLNMLNLENWTDLGSTVSQLERGLPUTRFMDNLEKETDOWVRQEM	109	:	:
QY	258	SKDLEEVKAAGVPYLDDFOKKWOBEMEYLRYKVPEPLRAELQEGARQKLHELQEKLSPUGE	317	:	:
Db	110	NKDLEEVKKGVQVPYLDDEFOKKWEDVELYRKVAPLGAELOESARQKLQELQGRLSPVAAE	169	:	:
QY	318	EMRDRAHVDALRTHLAPYSDELQRRLAAREALKENGARGLAIFYHAKATEHLSTLSEK	377	:	:
Db	170	EFDNRMTHTVDSIRTLQAPHSQMRESLAQRRLAEKSN--PTLNEYHTTRAKTHUKLGEK	227	:	:
QY	378	AKPALEDLRQGLLPVLSEFKVSFLSALE	405	:	:
Db	228	ARPAGEDLRHSLMPLETIKTKAQAVIE	255	:	:

RESULT 15
S21830
apolipoprotein A-I - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 20-Feb-1995 #sequence_revision 22-May-1998 #text_change 13-Aug-1999
C:Accession: S21830
R:Trieu, V N.; Rohrer-Nuttler, P.; Black, D.D.
submitted to the EMBL Data Library, May 1991
A:Description: Sequence and developmental expression of porcine ApoA-I mRNA
A:Reference number: S21830
A:Accession: S21830
A:Molecule type: mRNA
A:Residues: 1-164 <TRI>
A:Cross-references: EMBL:X59414; NID:g1891; PIDN:CAA42050.1; PID:g1892
A:Experimental source: liver
C:Superfamily: apolipoprotein A-I
C:Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid metabolism

	Query Match	29.28;	Score 617.5;	DB 2;	Length 164;
	Best Local Similarity	76.5%;	pred. No. 1.9e-22;		
	Matches 124;	Conservative 14;	Mismatches 23;	Indels 1;	Gaps
QY	253	LRQEMSKDLEEVKAKVQPYLDLDFQKKWQOEMELRYQKVEPLRAELOEGARQKLIHEIQEKL	312		
Db					
	4	LRQEMSKDLEEVKKVQPYLDLDFQKKWQOEMETRYQKMAPLGAEFREGARQKVOELQEKL	63		
QY	313	SPLGCEMRDRARHVDALRTHLAPYSDELQRLLAARLEALKENGGARLARLYAHAKATEHLIS	372		
Db	64	SPLAELRSRLRAHVLEARQHVAPYSDDLQRMAARFALKKEGGS-LABYQAKAQEQLK	122		

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 30, 2003, 15:04:22 ; Search time 13 seconds
(without alignments)
1320.862 Million cell updates/sec

Title: US-09-990-087-17

Perfect score: 2118

Sequence: 1 MGHHHHHHIEGRKLLDND.....SFKVSFLSALEYTKKLNTQ 414

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1024	48.3	267	1 APAL_HUMAN	P02647 homo sapien
2	991.5	46.8	267	1 APAL_MACFA	P15568 macaca fasc
3	860.5	40.6	266	1 APAL_CANFA	P02648 canis famil
4	837	39.5	266	1 APAL_RABIT	P09809 oryctolagus
5	814	38.4	265	1 APAL_PIG	P18648 sus scrofa
6	798	37.7	265	1 APAL_BOVIN	P15497 bos taurus
7	701.5	33.1	265	1 APAL_TUPGS	Q18759 tupaia glis
8	653	30.8	264	1 APAL_MOUSE	Q00623 mus musculus
9	584	27.6	259	1 APAL_RAT	P04639 rattus norv
10	505.5	23.9	264	1 APAL_ANAPL	Q42296 anas platyr
11	491.5	23.2	264	1 APAL_CHICK	P08250 gallus gall
12	470.5	22.2	264	1 APAL_COTUA	P32918 coturnix co
13	350.5	16.5	429	1 APAL_MACFA	P33621 macaca fasc
14	339.5	16.0	401	1 APAL_PAPAN	Q28758 papio anubi
15	320.5	15.1	396	1 APAL_HUMAN	P06727 homo sapien
16	316.5	14.9	382	1 APAL_PIG	Q46409 sus scrofa
17	292.5	13.8	391	1 APAL_RAT	P02651 rattus norv
18	279	13.2	395	1 APAL_MOUSE	P06728 mus musculus
19	244	11.5	262	1 AP12_ONCMY	O42363 brachydanio
20	238	11.2	262	1 AP12_ONCMY	O57524 oncorhynch
21	228.5	10.8	262	1 AP11_ONCMY	O57523 oncorhynch
22	224	10.6	262	1 APAL_SALTR	Q91488 salmo trutt
23	222.5	10.5	1102	1 MYSC_CHICK	P29616 gallus gall
24	222	10.5	1972	1 MYHB_MOUSE	O08638 mus musculus
25	214	10.1	879	1 RA50_SULTO	Q96yr5 sulfolobus
26	213	10.1	2230	1 GOG4_HUMAN	Q13439 homo sapien
27	210	9.9	1976	1 MYHA_BOVIN	Q27991 bos taurus
28	209.5	9.9	1978	1 MYHB_CHICK	P10587 gallus gall
29	209	9.9	1972	1 MYHB_HUMAN	P35749 homo sapien
30	208.5	9.8	1934	1 MYH7_MESAU	Q9uzc8 mesocricetu
31	208	9.8	880	1 RA50_PYRAB	Q29230 pyrococcus
32	208	9.8	886	1 RA50_ARCFU	O29230 archaeoglob
33	208	9.8	978	1 RA50_AQUAE	O67124 aquifex aeo

34	207.5	9.8	1938	1 MYH4_RABIT	Q28641 oryctolagus
35	207	9.8	1972	1 MYHB_RABIT	P35748 oryctolagus
36	205.5	9.7	1935	1 MYH7_PIG	P79293 sus scrofa
37	205	9.7	1935	1 MYH7_HUMAN	P12883 homo sapien
38	205	9.7	1961	1 MYH9_RAT	O62812 rattus norv
39	204.5	9.7	1938	1 MYH9_AEQIR	P24733 aequipecten
40	204.5	9.7	1976	1 MYHA_HUMAN	P35580 homo sapien
41	203.5	9.6	1935	1 MYH7_RAT	P02564 rattus norv
42	203	9.6	986	1 GM13_CHICK	O62839 rattus norv
43	203	9.6	1959	1 MYH9_CHICK	P14105 gallus gall
44	203	9.6	1976	1 MYHA_RAT	O9jlt0 rattus norv
45	202	9.5	281	1 APE_BRARE	O42364 brachydanio

ALIGNMENTS

RESULT 1

APAL_HUMAN	STANDARD;	PRT;	267 AA.
ID	P02647;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Apolipoprotein A-I precursor (Apo-AI).		
GN	APOA1.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=84221405; PubMed=6328445;		
RA	Sharpe C.R., Sololi A., Shelley C.S., Lucero M.A., Shoulders C.C.,		
RA	Baralle F.E.;		
RT	"Human apolipoproteins AI, AII, CII and CIII. cDNA sequences and mRNA		
RT	abundance.";		
RL	Nucleic Acids Res. 12:3917-3932(1984).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=85026665; PubMed=6207999;		
RA	Seilhamer J.J., Protter A.A., Frossard P., Levy-Wilson B.;		
RT	"Isolation and DNA sequence of full-length cDNA and of the entire		
RT	gene for human apolipoprotein AI -- discovery of a new genetic		
RT	polymorphism in the apo AI gene.";		
RL	DNA 3:309-317(1984).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=83220822; PubMed=6406984;		
RA	Shoulders C.C., Kornblitt A.R., Munro B.S., Baralle F.E.;		
RT	"Gene structure of human apolipoprotein AI.";		
RL	Nucleic Acids Res. 11:2827-2837(1983).		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=83220772; PubMed=6304641;		
RA	Cheung P., Chan L.;		
RT	"Nucleotide sequence of cloned cDNA of human apolipoprotein A-I.";		
RL	Nucleic Acids Res. 11:3703-3715(1983).		
RN	[5]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=84119464; PubMed=6198645;		
RA	Law S.W., Brewer H.B. Jr.;		
RT	"Nucleotide sequence and the encoded amino acids of human		
RT	apolipoprotein A-I mRNA.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 81:66-70(1984).		
RN	[6]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=86008382; PubMed=2995392;		
RA	Law S.W., Brewer H.B. Jr.;		
RT	"Tangier disease. The complete mRNA sequence encoding for		
RT	preproapo-A-I.";		
RL	J. Biol. Chem. 260:12810-12814(1985).		
RN	[7]		

RP SEQUENCE FROM N.A.
RX MEDLINE=84016011; PubMed=6413973;
RA Karathanasis S.K., Zannis V.I., Breslow J.L.;
RT "Isolation and characterization of the human apolipoprotein A-I
gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:6147-6151(1983).
[8]
RP SEQUENCE FROM N.A.
RX MEDLINE=89377481; PubMed=2673706;
RA Meglilevsky N., Roobol C., Loriau R., Guillaume J.P., Jacobs P.,
RA Cravador A., Herzog A., Brouwers L., Scarso A., Gilles P.,
RA Holmquist L., Carlson L.A., Bollen A.;
RT "Production of human recombinant proapolipoprotein A-I in Escherichia
coli: purification and biochemical characterization.";
RL DNA 8:429-436(1989).
[9]
RP SEQUENCE FROM N.A. (VARIANT TANGIER).
RX MEDLINE=88196137; PubMed=3129297;
RA Makrides S.C., Ruiz-Opazo N., Hayden M., Nussbaum A.L., Breslow J.L.,
RA Zannis V.I.;
RT "Sequence and expression of Tangier apoA-I gene.";
RL Eur. J. Biochem. 173:465-471(1988).
[10]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
[11]
RP SEQUENCE OF 118-267 FROM N.A.
RX MEDLINE=83091059; PubMed=6294659;
RA Breslow J.L., Ross D., McPherson J., Williams H.W., Kurnit D.,
RA Nussbaum A.L., Karathanasis S.K., Zannis V.I.;
RT "Isolation and characterization of cDNA clones for human
apolipoprotein A-I.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6861-6865(1982).
[12]
RP SEQUENCE OF 19-27.
RX MEDLINE=83256553; PubMed=6409108;
RA Brewer H.B. Jr., Fairwell T., Kay L., Meng M., Ronan R., Law S.,
RA Light J.A.;
RT "Human plasma proapoA-I: isolation and amino-terminal sequence.";
RL Biochem. Biophys. Res. Commun. 113:626-632(1983).
[13]
RP SEQUENCE OF 25-267.
RX MEDLINE=7812731; PubMed=204308;
RA Brewer H.B. Jr., Fairwell T., Larue A., Ronan R., Houser A.,
RA Bronzert T.J.;
RT "The amino acid sequence of human APOA-I, an apolipoprotein isolated
from high density lipoproteins.";
RL Biochem. Biophys. Res. Commun. 80:623-630(1978).
[14]
RP SEQUENCE OF 25-267.
RX MEDLINE=75133493; PubMed=164450;
RA Baker H.N., Gotto A.M. Jr., Jackson R.L.;
RT "The primary structure of human plasma high density apolipoprotein
glutamine I (ApoA-I). II. The amino acid sequence and alignment of
cyanogen bromide fragments IV, III, and I.";
RL J. Biol. Chem. 250:2725-2738(1975).
[15]
RP SEQUENCE OF 25-56.
RX MEDLINE=88333387; PubMed=3047170;
RA Yui Y., Aoyama T., Morishita H., Takahashi M., Takatsu Y., Kawai C.;
RT "Serum prostacyclin stabilizing factor is identical to apolipoprotein
A-I (Apo A-I). A novel function of Apo A-I.";
RL J. Clin. Invest. 82:803-807(1988).
[16]
RP SEQUENCE OF 25-48.
RX MEDLINE=89380318; PubMed=2506184;
RA Manjunath P., Marcel Y.L., Uma J., Seidah N.G., Chretien M.,
RA Chapdelaine A.;
RT "Apolipoprotein A-I binds to a family of bovine seminal plasma
proteins.";
RL J. Biol. Chem. 264:16853-16857(1989).

RP SEQUENCE OF 25-43.
RX MEDLINE=88070603; PubMed=3120314;
RA Prioli R.P., Ordoas J.M., Rosenberg I., Schaeffer E.J.,
RA Pereira M.E.A.;
RT "Similarity of cruzin, an inhibitor of Trypanosoma cruzi
neuraminidase, to high-density lipoprotein.";
RL Science 238:1417-1419(1987).
[18]
RP SEQUENCE OF 25-42.
RC TISSUE=Heart;
RX MEDLINE=95203287; PubMed=7895732;
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
RT "The human myocardial two-dimensional gel protein database: update
1994.";
RL Electrophoresis 15:1459-1465(1994).
[19]
RP PALMITOYLATION.
RX MEDLINE=86140194; PubMed=3005308;
RA Hoeg J.M., Meng M.S., Ronan R., Fairwell T., Brewer H.B. Jr.;
RT "Human apolipoprotein A-I. Post-translational modification by fatty
acid acylation.";
RL J. Biol. Chem. 261:3911-3914(1986).
[20]
RP PROCESSING.
RX MEDLINE=83195100; PubMed=6405383;
RA Zannis V.I., Karathanasis S.K., Keutmann H.T., Goldberger G.,
RA Breslow J.L.;
RT "Intracellular and extracellular processing of human apolipoprotein
A-I: secreted apolipoprotein A-I isoprotein 2 is a propeptide.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:2574-2578(1983).
[21]
RP STRUCTURE BY NMR OF 190-209.
RX MEDLINE=96270776; PubMed=8664326;
RA Wang G., Treleaven W.D., Cushley R.J.;
RT "Conformation of human serum apolipoprotein A-I(166-185) in the
presence of sodium dodecyl sulfate or dodecylphosphocholine by 1H-NMR
and CD. Evidence for specific peptide-SDS interactions.";
RL Biochim. Biophys. Acta 1301:174-184(1996).
[22]
RP X-RAY CRYSTALLOGRAPHY (4.0 ANGSTROMS) OF 67-267.
RX MEDLINE=98024124; PubMed=9356442;
RA Borhani D.W., Rogers D.P., Engler J.A., Brouillette C.G.;
RT "Crystal structure of truncated human apolipoprotein A-I suggests a
lipid-bound conformation.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12291-12296(1997).
[23]
RP VARIANT MILANO.
RX MEDLINE=83109095; PubMed=6401735;
RA Weisgraber K.H., Rall S.C. Jr., Bersot T.P., Mahley R.W.,
RA Franceschini G., Sirtori C.R.;
RT "Apolipoprotein A-Milano. Detection of normal A-I in affected
subjects and evidence for a cysteine for arginine substitution in the
variant A-I.";
RL J. Biol. Chem. 258:2508-2513(1983).
[24]
RP VARIANT TANGIER.
RX MEDLINE=83300108; PubMed=6412234;
RA Schmitz G., Assmann G., Rall S.C. Jr., Mahley R.W.;
RT "Tangier disease: defective recombination of a specific Tangier
apolipoprotein A-I isoform (pro-apo A-I) with high density
lipoproteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:6081-6085(1983).
[25]
RP VARIANT NORWAY.
RX MEDLINE=84289383; PubMed=6432779;
RA Rall S.C. Jr., Weisgraber K.H., Mahley R.W., Ogawa Y., Fielding C.J.,
RA Utermann G., Haas J., Steinmetz A., Menzel H.J., Assmann G.;
RT "Abnormal lecithin:cholesterol acyltransferase activation by a human
apolipoprotein A-I variant in which a single lysine residue is
deleted.";
RL J. Biol. Chem. 259:10063-10070(1984).
[26]

RESULT 3

APAL_CANFA STANDARD; PRT; 266 AA.

AC P02648;

DT 21-JUL-1986 (Rel. 01, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Apolipoprotein A-I precursor (Apo-AI).

GN APOA1.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Flissipedia; Canidae; Canis.

OX NCBI_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=90132271; PubMed=2515239;

RA Luo C.-C., Li W.-H., Chan L.;

RT "Structure and expression of dog apolipoprotein A-I, E, and C-I

RT mRNAs: implications for the evolution and functional constraints of

RT apolipoprotein structure.";

RL J. Lipid Res. 30:1735-1746(1989).

RN [2]

RP SEQUENCE OF 25-266.

RX MEDLINE=82142425; PubMed=6801039;

RA Chung H., Randolph A., Reardon I., Heiriksion R.L.;

RT "The covalent structure of apolipoprotein A-I from canine high

RT density lipoproteins.";

RL J. Biol. Chem. 257:2961-2967(1982).

RN [3]

RP SEQUENCE OF 25-57 AND 262-265.

RX MEDLINE=76210910; PubMed=179887;

RA Nakai T., Whayne T.F., Tang J.;

RT "The amino- and carboxyl-terminal sequences of canine apolipoprotein

RT A-I.";

RL FEBS Lett. 64:409-411(1976).

RN [4]

RP SEQUENCE OF 25-37.

RC TISSUE=Heart;

RX MEDLINE=98163340; PubMed=9504812;

RA Dunn M.J., Corbett J.M., Wheeler C.H.;

RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of

RT dog heart proteins.";

RL Electrophoresis 18:2795-2802(1997).

CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF

CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING

CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR

CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).

CC -1- SUBCELLULAR LOCATION: Extracellular.

CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN

CC CHYLOMICRONS. SYNTHESIZED IN THE LIVER AND SMALL INTESTINE.

CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.

DR PIR: A03092; LPDGA1.

DR HSP; P02847; IAVI.

DR HSC-2DPAGE; P02648; DOG.

DR InterPro; IPR000074; Apolipoprotein.

DR Pfam; PF01442; Apolipoprotein; 1.

KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.

FT SIGNAL 1 18 BY SIMILARITY.

FT PROPEP 19 24 APOLOPOPROTEIN A-I.

FT CHAIN 25 266

FT DOMAIN 67 266 10 X APPROXIMATE TANDEM REPEATS.

FT REPEAT 67 88 1.

FT REPEAT 89 110 2.

FT REPEAT 111 121 3 (HALF-LENGTH).

FT REPEAT 122 143 4.

FT REPEAT 144 165 5.

FT REPEAT 166 187 6.

FT REPEAT 188 209 7.

FT REPEAT 210 231 8.

FT REPEAT 232 242 9 (HALF-LENGTH).

FT REPEAT 243 266 10.

FT CONFLICT 168 168 A -> G (IN REF. 2).

FT CONFLICT 202 202 E -> Q (IN REF. 2).

FT CONFLICT 235 235 E -> Q (IN REF. 2).

FT CONFLICT 264 266 NAO -> A (IN REF. 3).

SQ SEQUENCE 266 AA; 30196 MW; A3202620C28A869D CRC64;

Query Match 40.6%; Score 860.5; DB 1; Length 266;

Best Local Similarity 62.9%; Pred. No. 1.2e-32;

Matches 175; Conservative 26; Mismatches 34; Indels 43; Gaps 1;

QY 137 DELRQRLAARLEALKENGARLAAYHAKATEHLSLSEKAKPALEDRLQGLLPVLESFVK 196

DB 32 DRVKDLATVYDVKDSGRDYVAQFEASA----- 60

QY 197 SFLSALAEVYTKLNTQGTLLKLDNWDVSTFSKLRQGLGPTVQFWDNLEKETGLRQE 256

DB 61 -----LGKQINLKLLDNWDSLSVTYKLRQIGPTVQFWDNLEKETGLRQE 108

QY 257 MSKDLEEVKAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQEGARQKLHEQKLSPLG 316

DB 109 MSKDLEEVKQVQPYLDDFQKKWQEEVELYRQKVAPLGSELREGARQKLQELQKLSPLA 168

QY 317 EEMRDRARAHVDALRTHLAPYSDELQRLAARLEALKENGARLAAYHAKATEHLSLSE 376

DB 169 EELRDRARTHVDALRAQLAPYSDDLRLAARLEALKEGGASLAAYHARASEQLSALCE 228

QY 377 KAKPALEDRLQGLLPVLESFVKVSFLSALAEVYTKKLNQ 414

DB 229 KARPALEDRLQGLLPVLESFVKVSLLAAIDENYTKKLNQ 266

RESULT 4

APAL_RABIT STANDARD; PRT; 266 AA.

AC P09809;

DT 01-MAR-1989 (Rel. 10, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Apolipoprotein A-I precursor (Apo-AI).

GN APOA1.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=22AP AI; TISSUE=Small intestine;

RA Paraskevopoulou T.B., Kritis A., Zannis V.I.;

RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Intestine;

RX MEDLINE=88082866; PubMed=3121329;

RA Pan T.C., Hao O.L., Yamin T.T., Dai P.H., Chen B.S., Chen S.L.,

RA Kroon P.A., Chao Y.S.;

RT "Rabbit apolipoprotein A-I mRNA and gene. Evidence that rabbit

RT apolipoprotein A-I is synthesized in the intestine but not in the

RT liver.";

RL Eur. J. Biochem. 170:99-104(1987).

RN [3]

RP SEQUENCE OF 25-266.

RX MEDLINE=87030294; PubMed=3095115;

RA Yang C., Yang T., Pownall H.J., Gotto A.M. Jr.;

RT "The primary structure of apolipoprotein A-I from rabbit high-density

RT lipoprotein.";

RL Eur. J. Biochem. 160:427-431(1986).

CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF

CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING

CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR

CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).

CC -1- SUBCELLULAR LOCATION: Extracellular.

CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN

CC CHYLOMICRONS.

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

```
CC -----
CC EMBL; L00626; AAA30992.1; -.
CC DR EMBL; X69477; CAA49234.1; -.
CC DR EMBL; X17057; -: NOT_ANNOTATED_CDS.
CC DR EMBL; X59414; CAA2050.1; -.
CC DR PIR; J00704; J00704.
CC DR PIR; A05311; A05311.
CC DR PIR; A46018; A46018.
CC DR PIR; S21830; S21830.
CC DR PIR; S31394; S31394.
CC DR HSP; P02647; IAV1.
CC DR InterPro; IPR00074; Apolipoprotein.
CC KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
CC FT SIGNAL 1 18 BY SIMILARITY.
CC FT PROPEP 19 24 APOLIPOPROTEIN A-I.
CC FT CHAIN 25 265 10 X APPROXIMATE TANDEM REPEATS.
CC FT DOMAIN 67 88 1.
CC FT REPEAT 89 110 2.
CC FT REPEAT 111 121 3 (HALF-LENGTH).
CC FT REPEAT 122 142 4.
CC FT REPEAT 144 165 5.
CC FT REPEAT 166 187 6.
CC FT REPEAT 188 209 7.
CC FT REPEAT 210 230 8.
CC FT REPEAT 231 241 9 (HALF-LENGTH).
CC FT REPEAT 242 265 10.
CC FT CONFLICT 108 108 E -> K (IN REF. 3).
CC FT CONFLICT 143 143 MISSING (IN REF. 2 AND 3).
CC FT CONFLICT 173 173 D -> S (IN REF. 4).
CC FT CONFLICT 180 180 E -> A (IN REF. 2 AND 3).
CC FT CONFLICT 185 186 HV -> QL (IN REF. 1 AND 5).
CC FT CONFLICT 209 209 G -> D (IN REF. 2 AND 3).
CC FT CONFLICT 224 224 A -> G (IN REF. 4).
CC FT CONFLICT 224 224 A -> G (IN REF. 4).
CC SEQUENCE 265 AA; 30325 MW; 2C6E578318ECF69C CRC64;

Query Match 38.4%; Score 814; DB 1; Length 265;
Best Local Similarity 59.9%; Pred. No. 1.4e-30;
Matches 167; Conservative 29; Mismatches 37; Indels 46; Gaps 3;

QY 137 DELRRLAARLEAKENGKARLAHYHAKAT-EHLSTLSERAKPALEDLROGLLPVLESFK 195
Db 32 DRVKDFATVYVDVDAIKDSGRDYVAQFEASALGKHLN----- 66

QY 196 YSFLSALEEYTKKLTQGTLLKLDNWDVSTFTSKRLRDLGPVTQEFWDNLEKETEGLRQ 255
Db 67 -----LKLNDWDSIGSTFTKVRDLGPVTQEFWDNLEKETEARLQ 107

Y 256 EMSKDLEEVKARVQPYLDDFKKQWEEMLYRQKVEPLRAELQCARQKHELEQKLSPL 315
Db 108 ENSKDLEEVKKVQPYLDDFQNKQWEEMLYRQKMAPLGAEFREGARQKVELEKLSPL 167

QY 316 GEEMDRARAHVDALRTHLAPYSDELRLAARLEAKENGKARLAHYHAKATHELTLS 375
Db 168 ABELDRRLAARLEAKENGKARLAHYHAKATHELTLS 375

QY 376 EKAKPALEDLROGLLPVLESFKVSVLSALEEYTKKLTQ 414
Db 227 EKAKPALEDLROGLLPVLENLKVLSILAAIDEASKLNQA 265

RESULT 6
APAL_BOVIN
ID APAL_BOVIN STANDARD; PRT; 265 AA.
AC P15497;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Apolipoprotein A-I precursor (Apo-AI).
GN APOA1.
```

Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
[1]
SEQUENCE FROM N.A.
MEDLINE=90348478; PubMed=2117227;
O'Huigin C., Chan L., Li W.H.;
"Cloning and sequencing of bovine apolipoprotein A-I cDNA and
molecular evolution of apolipoproteins A-I and B-100";
Mol. Biol. Evol. 7:327-339(1990).
[2]
SEQUENCE OF 19-265.
MEDLINE=92153895; PubMed=1739745;
Sparrow D.A., Lee B.R., Laplaud M.P., Auboliron S., Bauchart D.,
Chapman J.M., Gatto A.M. Jr., Yang C.Y., Sparrow J.T.;
"Plasma lipid transport in the preruminant calf, Bos spp: primary
structure of bovine apolipoprotein A-I";
Biochim. Biophys. Acta 1123:145-150(1992).
[3]
SEQUENCE OF 25-70.
MEDLINE=90147795; PubMed=2105728;
Auboliron S., Sparrow D.A., Beaubatie L., Bauchart D., Sparrow J.T.,
Laplaud M.P., Chapman J.M.;
"Characterization and amino-terminal sequence of apolipoprotein AI
from plasma high density lipoproteins in the preruminant calf, Bos
spp.";
Biochem. Biophys. Res. Commun. 166:833-839(1990).
-!- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
THE LECTIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
-!- SUBCELLULAR LOCATION: Extracellular.
-!- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
CHYLOMICRONS.
-!- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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EMBL; M35870; AAA30381.1; -.
PIR; A34649; A34649.
HSP; P02647; IAV1.
InterPro: IPR00074; Apolipoprotein.
Pfam; PF01442; Apolipoprotein; 1.
Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
SIGNAL 1 18
FT PROPEP 19 24 APOLIPOPROTEIN A-I.
FT CHAIN 25 265 10 X APPROXIMATE TANDEM REPEATS.
FT DOMAIN 67 88 1.
FT REPEAT 89 110 2.
FT REPEAT 111 121 3 (HALF-LENGTH).
FT REPEAT 122 143 4.
FT REPEAT 144 165 5.
FT REPEAT 166 187 6.
FT REPEAT 188 209 7.
FT REPEAT 210 230 8.
FT REPEAT 231 241 9 (HALF-LENGTH).
FT REPEAT 242 265 10.
FT CONFLICT 185 186 QL -> HV (IN REF. 2).
FT CONFLICT 185 186
SQ SEQUENCE 265 AA; 30276 MW; 06A2681EA2ABA50F CRC64;

Query Match 37.7%; Score 798; DB 1; Length 265;
Best Local Similarity 58.6%; Pred. No. 7.5e-30;
Matches 163; Conservative 28; Mismatches 43; Indels 44; Gaps 2;


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QY 137 DELRQRLAARLEALKENGARLAHYHAKATEHLSTLSEKAKPALEDLROGLLPVLESFKV 196
Db 32 DRVKDFATVVEAIKDSGRDYVAQFEASA----- 60
QY 197 SFLSALEYTKKLTQGTLLKLDNDWSDVSTFSKLRQGLPVTQEFWDNLEKETEGLRQE 256
Db 61 -----LGKQLNLKLDNDWDTLASTLSKVRQGLPVTQEFWDNLEKETASLRQE 108
QY 257 MSKDLEEVKAKVQPYLDQFKKWOEMELYRQKVEPLRAELOEGAROKLHELQKLSPLG 316
Db 109 MKHDLSEVKQVQPYLDQFKKWOEMELYRQKVEPLRAELOEGAROKLHELQKLSPLA 168
QY 317 EEMDRARAHVDALRTHLAPYSDELRLQRLAARLEALKENGARLAHYHAKATEHLSTLSE 376
Db 169 QELDRARAHVETLRQALAPYSDDLRLQRLAARLEALKENGARLAHYHAKATEHLSTLSE 227
QY 377 KAKPALEDLROGLLPVLESFKVSALEYTKKLTQ 414
Db 228 KAKPVLDELROGLLPVLESFKVSALEYTKKLTQ 265

RESULT 7
APAL_TUPGB STANDARD; PRT; 265 AA.
AC O18759;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Apolipoprotein A-I precursor (Apo-AI).
GN APOA1.
OS Tupaiia glis belangeri (Common tree shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Scandentia; Tupalidae; Tupaiia.
OX NCBI_TaxID=9396;
RN [1]
RC TISSUE=Liver;
RA Lu X., Chen B., Zhao Y., Wang K., Xue H., Zeng W.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR
CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
CC CHYLOMICRONS (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF005638; AAB92326.1; -.
DR HSSP; P02647; IAV1.
DR InterPro; IPR000074; Apolipoprotein.
DR Pfam; PF01442; Apolipoprotein; 1.
KW plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
FT SIGNAL 1 18
FT PROPEP 19 24
FT CHAIN 25 265
FT DOMAIN 67 265
FT REPEAT 67 88
FT REPEAT 89 110
FT REPEAT 111 121
FT REPEAT 122 143
FT REPEAT 144 165
FT REPEAT 166 187
FT REPEAT 188 209
FT REPEAT 210 231
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FT REPEAT 232 242
FT REPEAT 243 265
SQ SEQUENCE 265 AA; 30332 MW; 60076BC39FAEA165 CRC64;
Query Match 33.1%; Score 701.5; DB 1; Length 265;
Best Local Similarity 50.9%; Pred. No. 1.5e-25;
Matches 140; Conservative 41; Mismatches 51; Indels 43; Gaps 2;
QY 137 DELRQRLAARLEALKENGARLAHYHAKATEHLSTLSEKAKPALEDLROGLLPVLESFKV 196
Db 32 DRVDRLANVYDAVKESG-----REVVSQLEASA----- 60
QY 197 SFLSALEYTKKLTQGTLLKLDNDWSDVSTFSKLRQGLPVTQEFWDNLEKETEGLRQE 256
Db 61 -----LGKQLNLKLDNDWDTLGSTFKVHEHGLGVAQEFKLEKETELRRE 108
QY 257 MSKDLEEVKAKVQPYLDQFKKWOEMELYRQKVEPLRAELOEGAROKLHELQKLSPLG 316
Db 109 INKLEDEVROKTFQFLDEIQKKWOEDLERYRQKVEPLSAQLREGAROKLHELQKLVPLG 168
QY 317 EEMDRARAHVDALRTHLAPYSDELRLQRLAARLEALKENGARLAHYHAKATEHLSTLSE 376
Db 169 EDLRSVRAVADTLRTOLAPYSEQMRKTLGARLEAIKEGGSASLAHYHAKASEQLSALGE 228
QY 377 KAKPALEDLROGLLPVLESFKVSALEYTKKLT 411
Db 229 KAKPVLDEIHQGLMPWSEFKTGLVNLVIDEAAKKL 263

RESULT 8
APAL_MOUSE STANDARD; PRT; 264 AA.
AC Q00623;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apolipoprotein A-I precursor (Apo-AI).
GN APOA1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC TISSUE=Liver;
RA Scofield W., Mueller R., Binczek E., Hofmann K.;
RL "Mouse apolipoprotein AI. cDNA-derived primary structure, gene
RL organisation and complete nucleotide sequence.";
RL Biol. Chem. Hoppe-Seyler 373:187-193(1992).
RN [2]
RC TISSUE=Liver;
RA Januzzi J.L., Azrolan N., O'Connell A., Aalto-Setälä K., Breslow J.L.;
RL "Characterization of the mouse apolipoprotein ApoA-1/Apoc-3 gene
RL locus: genomic, mRNA, and protein sequences with comparisons to other
RL species.";
RL Genomics 14:1081-1088(1992).
RN [3]
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR
CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
CC CHYLOMICRONS.
CC -!- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
CC -----
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QY 318 EMRDRARAHVDAURTHLAPYSDELRLORLAARLEAKENGARLAHYHAKATEHLSTLSEK 377
 DB 166 EFPRDMRVNADALRAKFGLYSDQMRNLAQRLTEIRNH--PTLIEYTHKAGDHLRLYGEK 223
 QY 378 AKPALEDLRQGLLPVLESFVSFSLAEYTKKLN 412
 DB 224 AKPALDDLQGLMPVLEAWKAKIMSMIDEAKKLN 258

RESULT 10
 APALANAPL STANDARD; PRT; 264 AA.
 AC 042296;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1.
 OS Anas platyrhynchos (Domestic duck).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
 OX NCBI_TaxID=8839;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Pekin breed; TISSUE=Liver;
 RA Chen B., Lu X., Wang K., Xue H., Zeng W., Zhu D., Chi L.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
 CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
 CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR
 CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -!- SUBCELLULAR LOCATION: Extracellular.
 CC -!- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
 CC CHYLOMICRONS.
 CC -!- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; U86131; AAB64381.1; .
 CC DR HSSP; P02647; 1GW4.
 CC DR InterPro: IPR000074; Apolipoprotein.
 CC DR Pfam: PF01442; Apolipoprotein; 1.
 CC KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 CC FT SIGNAL 1 18 BY SIMILARITY.
 CC FT PROPEP 19 24 BY SIMILARITY.
 CC FT CHAIN 25 264 APOLOPOPROTEIN A-I.
 CC FT DOMAIN 67 264 10 X APPROXIMATE TANDEM REPEATS.
 CC FT REPEAT 67 88 1.
 CC FT REPEAT 89 110 2.
 CC FT REPEAT 111 121 3. (HALF-LENGTH).
 CC FT REPEAT 122 143 4.
 CC FT REPEAT 144 165 5.
 CC FT REPEAT 166 187 6.
 CC FT REPEAT 188 209 7.
 CC FT REPEAT 210 231 8.
 CC FT REPEAT 232 242 9. (HALF-LENGTH).
 CC FT REPEAT 243 264 10.
 CC SQ SEQUENCE 264 AA; 30659 MW; 7546F4BAF2846900 CRC64;

Query Match 23.9%; Score 505.5; DB 1; Length 264;
 Best Local Similarity 43.9%; Pred. No. 9e-17;
 Matches 104; Conservative 49; Mismatches 83; Indels 1; Gaps 1;

QY 174 EKAKPALEDLRQGLLPVLESFVSFSLAEY-TKKLNTQGLTKLNDWSDVTSTFKLR 232
 DB 25 DEFPALDRDLRDVLYLETKVASKGDKIAQFAEAVGKQLDLKADNLDTIGAAAKLR 84

QY 233 EOLGPVTOEFDWNLEKETEGRLQEMSKDLSEVKAKVOPVLDLDDFOKKWQEEEMELYRQKVEP 292
 DB 85 EDMAPIYKEVREMLWKDTESLRAELTKDLEEVKEKIRPFLDQFSKATKEELEYRQRLAP 144
 QY 293 LRAELOEGRKHLHELOKLSPLGEEMDRARAHVDALRTHLAPYSDELQRLAARLEAL 352
 DB 145 VAEELKELTKOKVLMQOKLTPVAEARDRLRGHVEELRNKLNAPYSDELKQLSQKLEEI 204
 QY 353 KENGARLAAYHAKATEHLSTLSEKAPALEDLQGLLPVLESFVSFSLAEYTK 409
 DB 205 REKGIPQAAYQAKVVEQLSNREKMTPLVDQFKERLTPYAENLKTFRISLLDELQK 261

RESULT 11
 APALCHICK STANDARD; PRT; 264 AA.
 AC P08250;
 DT 01-AUG-1998 (Rel. 08, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88049703; PubMed=3118875;
 RA Byrnes L., Luo C.-C., Li W.-H., Yang C.-Y., Chan L.;
 RT "Chicken apolipoprotein A-I: cDNA sequence, tissue expression and
 RT evolution.";
 RL Biochem. Biophys. Res. Commun. 148:485-492(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88152500; PubMed=3126099;
 RA Ferrari S., Tarugi P., Drusiani E., Calandra S., Fregni M.;
 RT "The complete sequence of chick apolipoprotein AI mRNA and its
 RT expression in the developing chick.";
 RL Gene 60:39-46(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87222301; PubMed=3108248;
 RA Rajavashisth T.B., Dawson P.A., Williams D.L., Shackelford J.E.,
 RA Leberer H., Lusis A.J.;
 RT "Structure, evolution, and regulation of chicken apolipoprotein A-I.";
 RL J. Biol. Chem. 262:7058-7065(1987).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92381402; PubMed=1512510;
 RA Lamoni-Fava S., Sastry R., Ferrari S., Rajavashisth T.B.,
 RA Lusis A.J., Karathanasis S.K.;
 RT "Evolutionary distinct mechanisms regulate apolipoprotein A-I gene
 RT expression: differences between avian and mammalian apoA-I gene
 RT transcription control regions.";
 RL J. Lipid Res. 33:831-842(1992).
 RN [5]
 RP SEQUENCE OF 25-44.
 RX MEDLINE=83213468; PubMed=6406496;
 RA Shackelford J.E., Leberer H.G.;
 RT "Synthesis and secretion of apolipoprotein AI by chick breast
 RT muscle.";
 RL J. Biol. Chem. 258:7175-7180(1983).
 CC -!- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
 CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
 CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR
 CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -!- SUBCELLULAR LOCATION: Extracellular.
 CC -!- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
 CC CHYLOMICRONS.
 CC -!- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.

[10]
 RP VARIANTS.
 RX MEDLINE-91310615; PubMed-1677358;
 RA Lohse P., Kindt M.R., Rader D.J., Brewer H.B. Jr.;
 RT "Three genetic variants of human plasma apolipoprotein A-IV: apoA-IV-1 (Thr-347-->Ser), apoA-IV-0 (Lys-167-->Glu, Gln-360-->His), and apoA-IV-3 (Glu-165-->Lys).";
 RL J. Biol. Chem. 266:13513-13518(1991).
 [11]
 RP ERRATUM.
 RA Lohse P., Kindt M.R., Rader D.J., Brewer H.B. Jr.;
 RL J. Biol. Chem. 266:19866-19866(1991).
 [12]
 RP VARIANT MET-13.
 RX MEDLINE-92238494; PubMed-1349197;
 RA von Eckardstein A., Funke H., Schulte M., Erren M., Schulte H., Assmann G.;
 RT "Nonsynonymous polymorphic sites in the apolipoprotein (apo) A-IV gene are associated with changes in the concentration of apo B- and apo A-I-containing lipoproteins in a normal population.";
 RL Am. J. Hum. Genet. 50:1115-1128(1992).
 [13]
 RP VARIANT SER-147.
 RX MEDLINE-92144647; PubMed-1737067;
 RA Tenkanen H., Koskinen P., Metso J., Baumann M., Lukka M., Kauppinen-Makelin R., Kontula K., Taskinen M.R., Manttari M., Manninen V., Ehnholm C.;
 RT "A novel polymorphism of apolipoprotein A-IV is the result of an asparagine to serine substitution at residue 127.";
 RL Biochim. Biophys. Acta 1138:27-33(1992).
 [14]
 RP VARIANT A-IV*5.
 RX MEDLINE-93136374; PubMed-1487136;
 RA Kamboh M.I., Williams E.R., Law J.C., Aston C.E., Bunker C.H., Ferrell R.E., Pollitzer W.S.;
 RT "Molecular basis of a unique African variant (A-IV 5) of human apolipoprotein A-IV and its significance in lipid metabolism.";
 RL Genet. Epidemiol. 9:379-388(1992).
 [15]
 RP VARIANT BUDAPEST-2 LYS-44; BUDAPEST-1 CYS-305 AND SER-367.
 RX MEDLINE-95245341; PubMed-7728150;
 RA Menzel H.J., Dieplinger H., Sandholzer C., Karadi I., Utermann G., Csaszar A.;
 RT "Apolipoprotein A-IV polymorphism in the Hungarian population: gene frequencies, effect on lipid levels, and sequence of two new variants.";
 RL Hum. Mutat. 5:58-65(1995).
 [16]
 RP VARIANTS FCHL SEATTLE SER-161; LEU-178 AND GLN-264.
 RX MEDLINE-97114287; PubMed-8956036;
 RA Deeb S.S., Nevin D.N., Iwasaki L., Brunzell J.D.;
 RT "Two novel apolipoprotein A-IV variants in individuals with familial combined hyperlipidemia and diminished levels of lipoprotein lipase activity.";
 RL Hum. Mutat. 8:319-325(1996).
 [17]
 RP FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION AND CATABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN LIPASE BY APOC-II: POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR COMPONENT OF HDL AND CHYLOMICRONS.
 [18]
 RP SUBCELLULAR LOCATION: Extracellular.
 [19]
 RP TISSUE SPECIFICITY: SYNTHESIZED PRIMARILY IN THE INTESTINE. SECRETED IN PLASMA.
 [20]
 RP DOMAIN: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS (EACH 22-MER IS ACTUALLY A TANDEM ARRAY OF TWO, A AND B, RELATED 11-MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-HELICAL, AND MANY OF THESE HELICES ARE AMPHIPATHIC. THEY MAY THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH LECITHIN:CHOLESTEROL ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.
 [21]
 RP POLYMORPHISM: EIGHT ALLELES HAVE BEEN CHARACTERIZED (APOA-IV*0 TO APOA-IV*7). APOA-IV*1 IS THE MAJOR ALLELE (90%), IV*2 IS ALSO COMMON (8%). THE OTHERS ARE RARE ALLELES.
 [22]
 RP DISEASE: DEFECTS IN APOA4 MAY CONTRIBUTE, ALONG WITH DEFECTS IN OTHER GENES OR ENVIRONMENTAL FACTORS, TO THE DEVELOPMENT OF

CC CC
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
 CC
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 CC
 CC EMBL: M14642; AAA51745.1;
 DR EMBL: X13629; CAA31955.1;
 DR EMBL: M14566; AAA51748.1;
 DR EMBL: J02758; AAA96731.1;
 DR EMBL: M13654; AAA51744.1;
 DR PIR: A26481; LPHUA4.
 DR PIR: A24449; A24449.
 DR PIR: A29330; A29330.
 DR PIR: A26280; A26280.
 DR PIR: S02715; S02715.
 DR HSP: P02649; ILE4.
 DR SWISS-2DPAGE; P06727; HUMAN.
 DR Genew; HGNC:602; APOA4.
 DR MTM: 107690;
 DR InterPro; IPR000074; Apolipoprotein.
 DR Pfam; PF01442; Apolipoprotein; 2.
 DR Plasma; Lipid transport; HDL; Chylomicron; Repeat; Signal;
 KW Disease mutation; Polymorphism.
 FT SIGNAL 1 20
 FT CHAIN 21 396
 FT DOMAIN 33 330
 FT REPEAT 33 54
 FT REPEAT 60 81
 FT REPEAT 82 103
 FT REPEAT 115 136
 FT REPEAT 137 158
 FT REPEAT 159 180
 FT REPEAT 181 202
 FT REPEAT 203 224
 FT REPEAT 225 246
 FT REPEAT 247 268
 FT REPEAT 269 286
 FT REPEAT 287 308
 FT REPEAT 309 330
 FT DOMAIN 372 389
 FT VARIANT 13 13
 FT VARIANT 44 44
 FT VARIANT 147 147
 FT VARIANT 161 161
 FT
 CC Query Match 15.1%; Score 320.5; DB 1; Length 396;
 CC Best Local Similarity 22.8%; Pred. No. 2.6e-08;
 CC Matches 87; Conservative 75; Mismatches 133; Indels 87; Gaps 7;
 QY 17 DNWDSVTSFSLKREQLGPGVPTQEFWDLNKEGRLQKQKAEVKAQVQVLDFOKK 76
 DB 64 DKLGIVNTYAGDLOKKLVFATFELHERLAKDSEKLEKEIGKEELERARLLPHANEVSK 123
 QY 77 WQEMELYFQKVEPLRAELQEGAROKHLQELKPLSGEMDRARAHVDALRTHLAPYS 136
 DB 124 IGDNLRELQORLEPYADQLRTQVNTQAEQLRRLQTPYAQMERMVLRNADSLQASLRPHA 183
 QY 137 DELRQRLARLEALEKNGARLAELHAKATEHLSTLSEKAKPALEDLROGLLPVLESKV 196
 DB 184 DELKADQNVELEKGR-----LTPYADEFKV 210
 QY 197 SFLSALEYTKKLNITQGLKLLDNWDSVTSFSLKREQLGPGVPTQEFWDLNKEGRLQ 256
 DB 211 -----KIDQTVLELRSLAPYAQDTQEKLNHLEGLTFQ 244

QY 257 MSKDLEEVKAKVOPYLDDFOKQWQEMELYRQKVEPLRAELQEGARQKLHELQEKLSPLG 316
Db 245 MKNNAEELKARISASAEEL-----RQRIAPLAEDVRGNLKGNTGLOKSLAELG 293
QY 317 EEMRDRARAHVDALRTHLAPYSDELQRLAARLEALKENGARLAIEYHAKATE-HLSTLS 375
Db 294 GHLDQ-----VEEFRRRVEPYGENFNKALVQOMEQLRQKLG-----HAGDVEGHLSFLE 344
QY 376 EAKPALEDLRQGLLPVLESFK 397
Db 345 -----KDLRDKVNSFFSTFK 359

Search completed: April 30, 2003, 15:12:03
Job time : 14 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 30, 2003, 15:09:57 ; Search time 87 Seconds
(without alignments)
980.500 Million cell updates/sec

Title: US-09-990-087-17
Perfect score: 2118
Sequence: 1 MGHHHHHIEGRLLDNWD.....SFKVSFLSALEYTKKLNQ 414

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp.archaea.*
- 2: sp.bacteria.*
- 3: sp.fungi.*
- 4: sp.human.*
- 5: sp.invertebrate.*
- 6: sp.mammal.*
- 7: sp.mhc.*
- 8: sp.organelle.*
- 9: sp.phage.*
- 10: sp.plant.*
- 11: sp.podent.*
- 12: sp.virus.*
- 13: sp.vertebrate.*
- 14: sp.unclassified.*
- 15: sp.rvirus.*
- 16: sp.bacteriap.*
- 17: sp.archeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	741.5	35.0	264	11 Q922L4	Q922L4 mesocricetu
2	644.5	30.4	263	11 Q08855	Q08855 mus musculu
3	643.5	30.4	263	11 Q03042	Q03042 mus musculu
4	614	29.0	241	6 Q9TS49	Q9TS49 erinaceus e
5	582	27.5	258	11 Q09054	Q09054 rattus norv
6	580	27.4	258	11 Q08877	Q08877 rattus norv
7	340.5	16.1	366	13 Q93601	Q93601 gallus gall
8	327	15.4	67	4 Q9Y355	Q9Y355 homo sapien
9	283	13.4	435	11 Q01488	Q01488 mus musculu
10	275	13.0	395	11 Q91XF8	Q91XF8 mus musculu
11	272	12.8	395	11 Q9DBN0	Q9DBN0 mus musculu
12	251	11.9	1547	5 Q26471	Q26471 schistocerc
13	247	11.7	56	6 Q02762	Q02762 ovis aries
14	246	11.6	50	4 Q8TDB0	Q8TDB0 homo sapien
15	243.5	11.5	263	13 Q98TG6	Q98TG6 anguilla ja
16	233.5	11.0	244	4 Q13784	Q13784 homo sapien

17	225.5	10.6	1411	4 Q15075	Q15075 homo sapien
18	222	10.5	1935	5 Q4934	Q4934 loligo peal
19	222	10.5	1972	11 Q8R384	Q8R384 mus musculu
20	220	10.4	1344	5 Q9XVL5	Q9XVL5 schmidtea m
21	219.5	10.4	1410	4 Q14221	Q14221 homo sapien
22	219	10.3	1708	5 Q9U056	Q9U056 mytilus gal
23	218.5	10.3	1743	5 Q96063	Q96063 dugesia jap
24	217	10.2	1937	13 Q91BD4	Q91BD4 gallus gall
25	217	10.2	2310	5 Q9NKR1	Q9NKR1 leishmania
26	216.5	10.2	363	4 Q9UBJ3	Q9UBJ3 homo sapien
27	215.5	10.2	2354	5 Q9NKT9	Q9NKT9 leishmania
28	214	10.1	3187	11 Q63714	Q63714 rattus norv
29	212	10.0	623	4 Q9H2G3	Q9H2G3 homo sapien
30	211.5	10.0	1940	5 Q9U7E3	Q9U7E3 pecten maxi
31	211.5	10.0	2238	11 Q70365	Q70365 mus musculu
32	210.5	9.9	1390	4 Q8W2A3	Q8W2A3 homo sapien
33	210.5	9.9	1530	4 Q43241	Q43241 homo sapien
34	209.5	9.9	275	13 Q9PT02	Q9PT02 oncorhynch
35	209	9.9	1999	11 Q63731	Q63731 rattus norv
36	209	9.9	2138	5 Q9XZE3	Q9XZE3 amoeba prot
37	208	9.8	1931	13 Q42352	Q42352 cyprinus ca
38	206.5	9.7	1935	6 Q9BE39	Q9BE39 bos taurus
39	206.5	9.7	1935	11 Q91Z83	Q91Z83 mus musculu
40	206.5	9.7	1938	6 Q9BE40	Q9BE40 bos taurus
41	205.5	9.7	1498	4 Q8TDA9	Q8TDA9 homo sapien
42	205.5	9.7	1598	11 Q922D2	Q922D2 mus musculu
43	205.5	9.7	1935	6 Q9GKR1	Q9GKR1 sus scrofa
44	205.5	9.7	1939	6 Q9TV63	Q9TV63 sus scrofa
45	205.5	9.7	2007	13 Q02015	Q02015 gallus gall

ALIGNMENTS

RESULT 1

Q922L4	Q922L4	PRELIMINARY;	PRT;	264 AA.
ID	Q922L4;			
AC	Q922L4;			
DT	01-MAY-1999 (TrEMBLrel. 10, Created)			
DT	01-MAY-1999 (TrEMBLrel. 10, Last sequence update)			
DT	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)			
DE	Apolipoprotein A-I.			
GN	APOAI.			
OS	Mesocricetus auratus (Golden hamster).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;			
OC	Mesocricetus.			
OX	NCBI_TaxID=10036;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=GOLDEN SYRIAN; TISSUE=INTESTINE;			
RX	MEDLINE=99061559; PubMed=9843713;			
RA	Wu J.Y.J., Reeves S.K., Wang Y.R., Wu Y., Lei P.P., Lei K.Y.;			
RT	"zinc deficiency decreases plasma level and hepatic mRNA abundance of			
RT	apolipoprotein A-I in rats and hamsters.";			
RL	Am. J. Physiol. 275:CL516-CL525(1998).			
DR	EMBL; AF046919; AAC98484.1; -.			
DR	HSSP; P02647; IAV1.			
DR	InterPro; IPR000074; Apolipoprotein.			
DR	Pfam; PF01442; Apolipoprotein; 1.			
KW	Lipoprotein.			
SQ	SEQUENCE 264 AA; 30739 MW; 280B22F4C0F0B129 CRC64;			
Query Match 35.0%; Score 741.5; DB 11; Length 264;				
Best Local Similarity 63.5%; Pred. No. 5.3e-28;				
Matches 148; Conservative 30; Mismatches 44; Indels 11; Gaps 3;				
QY	191	LESFKVSFLSALE----	EY-----	TKKLTQGTLLKLLDNWDSVTSTFSKLRQLQGPVTQE 241
Db	34	VKDFATVYDVADKDSGREGVVSQFETSA	LQNLNLENWDTLGTGVRQLQGPVTQE 93	
QY	242	FWDNLEKETGLRQEMSKDLEEVKAKVPYLD	DDFOKKWQEEEMELYRQKVEPLRAELQSGA 301	

Db 94 FWDNLEKETEWLRNEMKDLVEVKAKVQYPLDQFQTKWQEEVALYRQKMEPLGALERDGA 153

Qy 302 RQKLHELOEKLSPGCEEMDRARAHVDALRTHLAPYSDELQRLAARLEALKENGARLA 361

Db 154 RQKLHELOEKLTPGLEDURRHRHVDALRTHLAPYSQDMRDLAERLAQLKDS--PTLA 211

Qy 362 EYHAKATEHLSTLSKAKPALEDLROGLLPVLESFKVSFLSALAEYTKKLNQ 414

Db 212 EYHAKATEHLSTLSKAKPALEDLROGLLPVLESFKVSFLSALAEYTKKLNQ 264

RESULT 2

O08855 PRELIMINARY; PRT; 263 AA.

AC O08855;

DT 01-JUL-1997 (Tremblrel. 04, Created)

DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE Apolipoprotein A-I.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=SPLEEN;

RX MEDLINE=98077648; PubMed=9415807;

RA Chiang A.N., Fan K.C., Shaw G.C., Yang U.C.;

RT "Repetitive elements in the third intron of murine apolipoprotein A-I gene.";

RL Biochem. Mol. Biol. Int. 43:989-996(1997).

DR EMBL; U79574; AAB58426.1; -

DR HSP; P02647; IAV1.

DR InterPro: IPR000074; Apolipoprotein.

DR Pfam: PF01442; Apolipoprotein; 1.

KW Lipoprotein.

SQ SEQUENCE 263 AA; 30544 MW; 7825DF7483A5B24A CRC64;

Query Match 30.4%; Score 644.5; DB 11; Length 263;

Best Local Similarity 59.0%; Pred. No. 1.9e-23;

Matches 128; Conservative 37; Mismatches 47; Indels 5; Gaps 3;

Qy 198 FLSALEEYTKKLNQGTGTLKLLDNWDSVTFTSKLRQLQGPVTOEFWDNLEKETEGLRQEM 257

Db 52 YVSQFE--SSSLGQQLNLNLENWDTLGTSTVSQLQERLGPLTRDFWDLNLEKETDQVROEM 109

Qy 258 SKDLEEVKAKVQYPLDQFQTKWQEEVALYRQKMEPLGALERDGA 317

Db 110 NKDLEEVKQVQYPLDQFQTKWQEEVALYRQKMEPLGALERDGA 168

Qy 318 EMRDRARAHVDALRTHLAPYSDELQRLAARLEALKENGARLAERHAKATEHLSTLSEK 377

Db 169 EFRDRMTHVDSLRTQLAPHSEQMSRLAQLAELKSN--PTLNEYHTRAKTHLKTGK 226

Qy 378 AKPALEDLROGLLPVLESFKVSFLSALAEYTKKLNQ 414

Db 227 ARPALEDLRLHSLMPLETLTKAQSVIDKASETLTAQ 263

RESULT 4

Q9TS49 PRELIMINARY; PRT; 241 AA.

AC Q9TS49;

DT 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)

DE Apolipoprotein A-I, APOA-I-CHOLESTEROL transporter.

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Insectivora; Erinaceidae; Erinaceus.

OX NCBI_TaxID=9365;

RN [1]

RP SEQUENCE.

RX MEDLINE=95294458; PubMed=7775860;

RA Sparrow D.A., Laplaud P.M., Saboureaux M., Zhou G., Dolphin P.J.,

RA Gotto A.M.Jr., Sparrow J.T.;

RT "Plasma lipid transport in the hedgehog: partial characterization of structure and function of apolipoprotein A-I.";

RL J. Lipid Res. 36:485-495(1995).

DR HSP; P02647; IAV1.

DR InterPro: IPR000074; Apolipoprotein.

DR Pfam: PF01442; Apolipoprotein; 1.

SQ SEQUENCE 241 AA; 27630 MW; 2EF00F2B69210535 CRC64;

Query Match 29.0%; Score 614; DB 6; Length 241;

Best Local Similarity 53.3%; Pred. No. 4.5e-22;

Matches 130; Conservative 35; Mismatches 73; Indels 6; Gaps 3;

Qy 174 EKAKPALEDLROGLLPVLESFKVS--FLSALAEYTKKLNQGTGTLKLLDNWDSVTSTFSK 230

Db 1 DEAKSYMDQIKDMLTVYDVTAKDSKDYLTSLD--TSALGQQLNKKLADNWDVSSALLK 58

Qy 231 LREQLGPVTOEFWDNLEKETEGLRQEMSKDLEEVKAKVQYPLDQFQTKWQEEVALYRQK 290

Db 59 AREQMKPIAMEFQWGNLEKDTGLRQTSKDLVLEKVKVQYPLDQFQTKWQEEVALYRQK 118

Qy 291 EPLRAELQEGARQKLHELOEKLSPGCEEMDRARAHVDALRTHLAPYSDELQRLAARLE 350

Db 119 APLSAWEQARQAKAELOQKAGELGQQRDRVRTHVDALRTDLAPYGEAKLLQRLQ 178

Db 94 FWDNLEKETEWLRNEMKDLVEVKAKVQYPLDQFQTKWQEEVALYRQKMEPLGALERDGA 153

Qy 302 RQKLHELOEKLSPGCEEMDRARAHVDALRTHLAPYSDELQRLAARLEALKENGARLA 361

Db 154 RQKLHELOEKLTPGLEDURRHRHVDALRTHLAPYSQDMRDLAERLAQLKDS--PTLA 211

Qy 362 EYHAKATEHLSTLSKAKPALEDLROGLLPVLESFKVSFLSALAEYTKKLNQ 414

Db 212 EYHAKATEHLSTLSKAKPALEDLROGLLPVLESFKVSFLSALAEYTKKLNQ 264

RESULT 3

O09042 PRELIMINARY; PRT; 263 AA.

AC O09042;

DT 01-JUL-1997 (Tremblrel. 04, Created)

DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)

DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)

DE Apolipoprotein A-I.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=SPLEEN;

RX MEDLINE=98077648; PubMed=9415807;

RA Chiang A.N., Fan K.C., Shaw G.C., Yang U.C.;

RT "Repetitive elements in the third intron of murine apolipoprotein A-I gene.";

RL Biochem. Mol. Biol. Int. 43:989-996(1997).

DR EMBL; U79574; AAB58426.1; -

DR HSP; P02647; IAV1.

DR InterPro: IPR000074; Apolipoprotein.

DR Pfam: PF01442; Apolipoprotein; 1.

KW Lipoprotein.

SQ SEQUENCE 263 AA; 30544 MW; 7825DF7483A5B24A CRC64;

Query Match 30.4%; Score 644.5; DB 11; Length 263;

Best Local Similarity 59.0%; Pred. No. 1.9e-23;

Matches 128; Conservative 37; Mismatches 47; Indels 5; Gaps 3;

Qy 198 FLSALEEYTKKLNQGTGTLKLLDNWDSVTFTSKLRQLQGPVTOEFWDNLEKETEGLRQEM 257

Db 52 YVSQFE--SSSLGQQLNLNLENWDTLGTSTVSQLQERLGPLTRDFWDLNLEKETDQVROEM 109

Qy 258 SKDLEEVKAKVQYPLDQFQTKWQEEVALYRQKMEPLGALERDGA 317

Db 110 NKDLEEVKQVQYPLDQFQTKWQEEVALYRQKMEPLGALERDGA 168

Qy 318 EMRDRARAHVDALRTHLAPYSDELQRLAARLEALKENGARLAERHAKATEHLSTLSEK 377

Db 169 EFRDRMTHVDSLRTQLAPHSEQMSRLAQLAELKSN--PTLNEYHTRAKTHLKTGK 226

Qy 378 AKPALEDLROGLLPVLESFKVSFLSALAEYTKKLNQ 414

Db 227 ARPALEDLRLHSLMPLETLTKAQSVIDKASETLTAQ 263

RESULT 3

O09042 PRELIMINARY; PRT; 263 AA.

AC O09042;

DT 01-JUL-1997 (Tremblrel. 04, Created)

DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)

DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)

DE Apolipoprotein A-I.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

QY 351 ALKENGARLAHYHAKATEHSTLSEKAKPALEDLROGLLPVLESFKYVSFLSALEYTKK 410
 Db 179 DIKAKSG-DLAHYQTKLSEHLKSFGEKAKPTQLDRLHGLEPLWEGIKAGAMSLBELGKK 237
 QY 411 LNTQ 414
 Db 238 LNSQ 241

RESULT 5
 ID O09054 PRELIMINARY; PRT; 258 AA.
 AC O09054;
 DT 01-JUL-1997 (TReMBLrel. 04, Created)
 DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE Apolipoprotein A-I.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-WKY, AND SHRSP; TISSUE-SPLEEN;
 RA Chiang A.N., Fan K.C., Shaw G.C., Yang U.C.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U79578; AAB58430.1; -
 DR EMBL; U79577; AAB58429.1; -
 DR HSSP; P02647; IAV1.
 DR InterPro; IPR000074; Apolipoprotein.
 DR Pfam; PF01442; Apolipoprotein; 1.
 KW Lipoprotein.
 SQ SEQUENCE 258 AA; 29918 MW; 093E6EF2E629CDC8 CRC64;

Query Match 27.5%; Score 582; DB 11; Length 258;
 Best Local Similarity 54.4%; Pred. No. 1.5e-20;
 Matches 117; Conservative 34; Mismatches 56; Indels 8; Gaps 3;

QY 198 FLSALEEYTKKLTQGTGLKLDNDVSTFSKLREQLGPGVPTQFWDNLEKETGLRQEM 257
 Db 51 YVSQESST--LGKQLNLNLDNDVSTGVRQLQEQGLGPTQDFWANLEKETDWPFRNM 108
 QY 258 SKDLEEVKAKVQPYLDDFOKKWQEMELYRQKVEPLRAELQEGARQKLHELQKLSPLGE 317
 Db 109 NKDLNVKQKQPHLDFQEKWNEEVEAYRQKLEPLATELHKNAK----EMQRHLKVVAE 164
 QY 318 EMRDRARAHVDALRTHLAPYSDELRLQRLAARLEALKENGARLAHYHAKATEHLSLSEK 377
 Db 165 EFRDMRVNADALRAKFGLYSDQMRNLAQRLTEIKNH--PTLIEYHTKASDHLKTLGK 222
 QY 378 AKPALEDLROGLLPVLESFKYVSFLSALEYTKKLN 412
 Db 223 AKPALDDLQGLMPVLEAWKAKINSMIDEAKKKLN 257

RESULT 6
 ID O08877 PRELIMINARY; PRT; 258 AA.
 AC O08877;
 DT 01-JUL-1997 (TReMBLrel. 04, Created)
 DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Apolipoprotein A-I.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SHR; TISSUE-SPLEEN;
 RA Chiang A.N., Fan K.C., Shaw G.C., Yang U.C.;
 RL MEDLINE=98077648; PubMed=9415807;
 RX MEDLINE=98077648; PubMed=9415807;
 RA Chiang A.N., Fan K.C., Shaw G.C., Yang U.C.;

RT "Repetitive elements in the third intron of murine apolipoprotein A-I
 gene.";
 RL Biochem. Mol. Biol. Int. 43:989-996(1997).
 DR EMBL; U79576; AAB58428.1; -
 DR HSSP; P02647; IAV1
 DR InterPro; IPR000074; Apolipoprotein.
 DR Pfam; PF01442; Apolipoprotein; 1.
 KW Lipoprotein.
 SQ SEQUENCE 258 AA; 29831 MW; 093FB582E629CDC8 CRC64;

Query Match 27.4%; Score 580; DB 11; Length 258;
 Best Local Similarity 54.4%; Pred. No. 1.9e-20;
 Matches 117; Conservative 33; Mismatches 57; Indels 8; Gaps 3;

QY 198 FLSALEEYTKKLTQGTGLKLDNDVSTFSKLREQLGPGVPTQFWDNLEKETGLRQEM 257
 Db 51 YVSQESST--LGKQLNLNLDNDVSTGVRQLQEQGLGPTQDFWANLEKETDWPFRNM 108
 QY 258 SKDLEEVKAKVQPYLDDFOKKWQEMELYRQKVEPLRAELQEGARQKLHELQKLSPLGE 317
 Db 109 NKDLNVKQKQPHLDFQEKWNEEVEAYRQKLEPLATELHKNAK----EMQRHLKVVAE 164
 QY 318 EMRDRARAHVDALRTHLAPYSDELRLQRLAARLEALKENGARLAHYHAKATEHLSLSEK 377
 Db 165 EFRDMRVNADALRAKFGLYSDQMRNLAQRLTEIKNH--PTLIEYHTKASDHLKTLGK 222
 QY 378 AKPALEDLROGLLPVLESFKYVSFLSALEYTKKLN 412
 Db 223 AKPALDDLQGLMPVLEAWKAKINSMIDEAKKKLN 257

RESULT 7
 ID O93601 PRELIMINARY; PRT; 366 AA.
 AC O93601;
 DT 01-NOV-1998 (TReMBLrel. 08, Created)
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Apolipoprotein AIV.
 GN APOAIV.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Callus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98221191; PubMed=95531114;
 RA Steinmetz A., Hermann M., Nimpf J., Aebersold R., Ducret A.,
 RA Weinberg R.B., Schneider W.J.;
 RT "Expression and conservation of apolipoprotein AIV in an avian
 species";
 RL J. Biol. Chem. 273:10543-10549(1998).
 DR EMBL; Y16534; CAA76273.1; -
 DR InterPro; IPR000074; Apolipoprotein.
 DR Pfam; PF01442; Apolipoprotein; 2.
 KW Lipoprotein.
 SQ SEQUENCE 366 AA; 40852 MW; B47DB49F3E8D91CE CRC64;

Query Match 16.1%; Score 340.5; DB 13; Length 366;
 Best Local Similarity 23.2%; Pred. No. 4.7e-09;
 Matches 91; Conservative 78; Mismatches 134; Indels 89; Gaps 6;

QY 15 LLDNDVSTFSKLREQLGPGVPTQFWDNLEKETGLRQEMSKDLEEVKAKVQPYLDDFQ 74
 Db 61 LOSNLOSANSYAEELQRLRPVFPATELQALQVODSQRLLKQIOQELAELOAKLAPYDEVH 120
 QY 75 KKWQEMELYRQKVEPLRAELQEGARQKLHELQKLSPLGEEMRDRARAHVDALRTHLAP 134
 Db 121 QQIGTNIRELOAKLSPYADELRSQVDRGTGELRRALEFPATELREKLDQNDADSIQSLGP 180
 QY 135 YSDELRLQRLAARLEALKENGARLAHYHAKATEHLSLSEKAKPALEDLROGLLPVLESF 194

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Db 181 YAEKQIDSSVEGLK-----GQLTFLADELKEQVAQSVGLRKG----- 221
QY 195 KVSFLSALEYTKLNTQGTKLKLDNWDVSTFSKLRQLGVPVTOFFWDLNLEKETEGLR 254
Db 222 -----LSPYAQEVQDGLNRQLQSLT 241
QY 255 QEMSKDLLEVKAKVQPYLDLDFQKKWOEMELYRQKVEPLRAELQEGARQKLHELOEKLSP 314
Db 242 AQMERAAEELRSIAAS-----SEEM---RAQLSPLAQELQEAALGRDAEAMQORLAP 290
QY 315 LGEMRDRARAHVDALRTHLAPYSDELQRRLAARLALKENGARLAAYHAKATEHLSTL 374
Db 291 LAQQLDERLAQTVFAFQQAQISFETPRQQLVQRLEEMQO-----KLESQTAGVEDHLDLL 346
QY 375 SEKAKPALEDLRQGLLPLVLESFKVSFLSALEE 406
Db 347 EKEVRKV-----ATFLSTTEQ 363

RESULT 8
QY355 PRELIMINARY; PRT; 67 AA.
AC QY355;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Apolipoprotein A1 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99216322; PubMed=10198255;
RA Hamidi Asl K., Liepnieks J.J., Nakamura M., Parker F., Benson M.D.;
RT "A novel apolipoprotein A-1 variant, Arg173pro, associated with
cardiac and cutaneous amyloidosis.";
RL Biochem. Biophys. Res. Commun. 257:584-588(1999).
DR EMBL; AF148963; AAD34604.1; -
DR HSP; P02647.1A1.
DR InterPro; IPR000074; Apolipoprotein.
DR Pfam; PF01442; Apolipoprotein; 1.
KW Lipoprotein.
FT NON_TER 1
FT NON_TER 67
FT NON_TER 67
SQ SEQUENCE 67 AA; 7433 MW; 525E1FEB7BDD5AFB CRC64;

Query Match 15.4%; Score 327; DB 4; Length 67;
Best Local Similarity 98.5%; Pred. No. 3.2e-09;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

312 LSPGLGEEMRDRARAHVDALRTHLAPYSDELQRRLAARLALKENGARLAAYHAKATEHL 371
1 LSPGLGEEMRDRARAHVDALRTHLAPYSDELQRRLAARLALKENGARLAAYHAKATEHL 60

QY 372 STLSEKA 378
Db 61 STLSEKA 67

RESULT 9
Q01488 PRELIMINARY; PRT; 435 AA.
AC Q01488;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Variant apolipoprotein A-IV precursor (APOA-IV).
GN APOA-4.
OS Mus musculus castaneus (southeastern Asian house mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10091;

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RN SEQUENCE FROM N.A.
RP MEDLINE=91286309; PubMed=1648102;
RA Reue K., Leete T.H.;
RT "Genetic variation in mouse apolipoprotein A-IV due to insertion and
deletion in a region of tandem repeats.";
RL J. Biol. Chem. 266:12715-12721(1991).
CC !- FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION AND
CATABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN
LIPASE BY APOC-II: POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR
COMPONENT OF HDL AND CHYLOMICRONS. IT MAY PLAY A ROLE IN THE
INTRAVASCULAR METABOLISM OF HDL. POTENTIAL ROLE IN CELLULAR
CHOLESTEROL EFFLUX.
CC !- TISSUE SPECIFICITY: INTESTINE, LIVER, AND PLASMA.
CC !- MISCELLANEOUS: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS
(EACH 22-MER IS ACTUALLY A TANDEM ARRAY OF TWO, A & B, RELATED 11-
MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-
HELICAL, & MANY OF THESE HELICES ARE AMPHIPATHIC. THEY MAY
THEREFORE SERVE AS LIPID -BINDING DOMAINS WITH
LECITHIN:CHOLESTEROL ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.
CC !- MISCELLANEOUS: THE APOA-IV POLYMORPHISMS ARE CLASSIFIED BASED ON
THE OCCURENCE OF THREE, FOUR, OR FIVE E-Q-A-Q/ E-Q-Q-Q/ E-Q-V-Q
REPEAT UNITS.
CC EMBL; M64250; AAA37216.1; -
DR InterPro; IPR000074; Apolipoprotein.
DR Pfam; PF01442; Apolipoprotein; 2.
KW Lipid transport; HDL; VLDL; Chylomicron; Repeat; Signal; Liver;
KW Plasma; Multigene family; Polymorphism; Cholesterol metabolism.
FT SIGNAL 1 20
FT CHAIN 21 435
FT DOMAIN 374 393
FT REPEAT 374 377 1.
FT REPEAT 378 381 2.
FT REPEAT 382 385 3.
FT REPEAT 386 389 4.
FT REPEAT 390 393 5.
FT REPEAT 435 AA; 49254 MW; B2AF55EEA8E456B2 CRC64;
SQ SEQUENCE 435 AA; 49254 MW; B2AF55EEA8E456B2 CRC64;

Query Match 13.4%; Score 283; DB 11; Length 435;
Best Local Similarity 22.7%; Pred. No. 2.8e-06;
Matches 83; Conservative 73; Mismatches 131; Indels 78; Gaps 7;

QY 24 STFSK-LRQLGVPVTOFFWDLNLEKETEGLRQEMSKDLLEVKAKVQPYLDLDFQKKWOEME 82
Db 70 STYADGVNRKLVFVVVQLSGHLAKETERVKEIKKELEDLRDRMMPHANKVTTQTGENMQ 129
QY 83 LYRQKVEPLRAELQEGARQKLHELOEKLSPGLGEEMRDRARAHVDALRTHLAPYSDELQR 142
Db 130 KLOEHLKPYAVDLQDINTQTQEMKQLQTPYIORMQTIKENVNLTHTSMPLATNLKDK 189
QY 143 LAARLALKENGARLAAYHAKATEHLSTLSEKAKPALEDLRQGLLPLVLESFKVSFLSAL 202
Db 190 FNRNMEELK-----GHLLTPRANELKATIDQN-----LEDLRR----- 221
QY 203 EETTKLNTQGTKLKLDNWDVSTFSKLRQLGVPVTOFFWDLNLEKETEGLRQEMSKOLE 262
Db 222 -----SLAPTVGVQEKLNHQMGLAFQMKNAE 250
QY 263 EVKAKVQPYLDLDFQKKWOEMELYRQKVEPLRAELQEGAR-----OKLHELOEKLSP 315
Db 251 ELQTKYSAKIDQLQKNLAPLVEDVQSKVGNTQGLQSKLDLNRQLEQOQVEEFRTVEPM 310
QY 316 GEEMRDRARAHVDALRTHLAPYSDELQRRLAARLALKENGARLAAYHAKATEHLSTLS 375
Db 311 GEMFNKALVQOQLEQFRQOLGPNSEGEVESHLSLFLEKSLRE-----KVNSEFMSTLE 359
QY 376 EKAKP 380
Db 360 KKQSP 364

RESULT 10
Q91XF8

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ID Q91XF8 PRELIMINARY; PRT; 395 AA.
AC Q91XF8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Unknown (protein for MGC:18592).
GN APOA4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010769; AAH10769.1; -.
DR MGD; MGI:88051; APOA4.
DR InterPro; IPR000074; Apolipoprotein.
DR Pfam; PF01442; Apolipoprotein; 2.
SQ SEQUENCE 395 AA; 45029 MW; C48BE32EED441F71 CRC64;

Query Match 13.0%; Score 275; DB 11; Length 395;
Best Local Similarity 22.2%; Pred. No. 6e-06;
Matches 81; Conservative 74; Mismatches 132; Indels 78; Gaps 7;

QY 24 STFSK-LRQOLGPVTOEFWDNLEKETEGLRQEMSKDLREVKAKVQPYLDDFOKKWOEME 82
DB 70 STYADGVHKNLVPFVQVLSGHLAQETERYKKEIKKELEDRLDRMPHANKVTQTGENMQ 129
QY 83 LYRQKVEPLRAELQEGARKHLEQKLSPLGEMDRARAHVDALRTHLAPYSDELQR 142
DB 130 KLQEHLPKPYAVDLDQINTQTEMKQLPTPIQRMQTTIKENVNLHTSMPLATNLKDK 189
QY 143 LAARLEALKENGARLAETHAKATEHLSTLSEKAPALDRLQGLLPVLESFKVSFLSAL 202
DB 190 FNRNMEELK-----GHLTPRANELKATIDQN-----LEDLRR----- 221
QY 203 EYTKKLTQGTLLKLDNDSDVTSTFSKLRQOLGPVTOEFWDNLEKETEGLRQEMSKDLE 262
DB 222 -----SLAPITGVQVQKLNHOMEGLAFOKKNAE 250
QY 263 EVKAKVQPYLDDFOKKWOEMELYRQKV----EPLRAELQEGAR---QKLHLEQKLSPL 315
DB 251 ELQTKVSAKIDQLQKNLAPLVEDVQSKVKGNTGEGLSLEDLNRLQEQVEEFRTVEPM 310
QY 316 GEEMDRARAHVDALRTHLAPYSDELQRQRLAARLEALKENGARLAETHAKATEHLSTLS 375
DB 311 GEMFNKALVQOLEQFROQLGPNSEGEVSHLSFLEKSLRE-----KYNFSFMSTLE 359
QY 376 EKAKP 380
DB 360 KKGSP 364

RESULT 11
Q9DBNO PRELIMINARY; PRT; 395 AA.
AC Q9DBNO;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Adult male liver cDNA, RIKEN full-length enriched library,
DE clone:1300002K10, full insert sequence.
GN APOA4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC TISSUE=LIVER;
RA STRAIN=C57BL/6J; TISSUE=LIVER;
RC MEDLINE=21085660; PubMed=11217851;

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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
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RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
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RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
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RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK004856; BAB23620.1; -.
DR MGD; MGI:88051; APOA4.
DR InterPro; IPR000074; Apolipoprotein.
DR Pfam; PF01442; Apolipoprotein; 2.
SQ SEQUENCE 395 AA; 45044 MW; 4102D84ACB0D182A CRC64;

Query Match 12.8%; Score 272; DB 11; Length 395;
Best Local Similarity 22.2%; Pred. No. 8.3e-06;
Matches 81; Conservative 73; Mismatches 133; Indels 78; Gaps 7;

QY 24 STFSK-LRQOLGPVTOEFWDNLEKETEGLRQEMSKDLREVKAKVQPYLDDFOKKWOEME 82
DB 70 STYADGVHKNLVPFVQVLSGHLAQETERYKKEIKKELEDRLDRMPHANKVTQTGENMQ 129
QY 83 LYRQKVEPLRAELQEGARKHLEQKLSPLGEMDRARAHVDALRTHLAPYSDELQR 142
DB 130 KLQEHLPKPYAVDLDQINTQTEMKQLPTPIQRMQTTIKENVNLHTSMPLATNLKDK 189
QY 143 LAARLEALKENGARLAETHAKATEHLSTLSEKAPALDRLQGLLPVLESFKVSFLSAL 202
DB 190 FNRNMEELK-----GHLTPRANELKATIDQN-----LEDLRR----- 221
QY 203 EYTKKLTQGTLLKLDNDSDVTSTFSKLRQOLGPVTOEFWDNLEKETEGLRQEMSKDLE 262
DB 222 -----SLAPITGVQVQKLNHOMEGLAFOKKNAE 250
QY 263 EVKAKVQPYLDDFOKKWOEMELYRQKV----EPLRAELQEGAR---QKLHLEQKLSPL 315
DB 251 ELQTKVSAKIDQLQKNLAPLVEDVQSKVKGNTGEGLSLEDLNRLQEQVEEFRTVEPM 310
QY 316 GEEMDRARAHVDALRTHLAPYSDELQRQRLAARLEALKENGARLAETHAKATEHLSTLS 375
DB 311 GEMFNKALVQOLEQFROQLGPNSEGEVSHLSFLEKSLRE-----KYNFSFMSTLE 359
QY 376 EKAKP 380
DB 360 KKGSP 364

RESULT 12
Q26471 PRELIMINARY; PRT; 1547 AA.
ID Q26471
AC Q26471;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE BLACKJACK protein.
OS Schistocerca americana (American grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
OC Acridomorpha; Acridoidea; Acrididae; Cyrtacanthacridinae;
OC Schistocerca.
OX NCBI_TaxID=7009;

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